

Sequence Listing

<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.

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<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature

<222> 36-47, 108-113, 166-171, 198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

<400> 10
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
1 5 10 15

Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
20 25 30

Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
35 40 45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60

Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75

Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120

Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
125 130 135

Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
140 145 150

Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
155 160 165

Gly Gly Arg Leu Ala Ile Val Gly Gly Tyr Thr Pro Ser Lys
170 175 180

Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
185 190 195

Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys
200 205 210

Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala
215 220 225

Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu
230 235 240

Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser
245 250 255

Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His
260 265 270

Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys
275 280 285

Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala
290 295 300

Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn
305 310 315

Pro Lys Ala Val

<210> 11
<211> 2720
<212> DNA
<213> Homo sapines

<400> 11
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gccctttggg ccgtcgccac cactgttagtc atgtaccac cggccggcc 150
gccgcctcat cgggacttca tctcggtgac gctgagctt ggcgagagct 200
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ttgatttgct ctaaccgcaa 2720

<210> 12
<211> 699
<212> PRT
<213> Homo sapiens

<220>
<221> TRANSMEM
<222> 21-40 and 84-105
<223> Transmembrane Domain (type II)

<400> 12
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Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
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Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro
35 40 45
His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
50 55 60
Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
65 70 75
Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
80 85 90
Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
95 100 105

Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys
 110 115 120
 Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val
 125 130 135
 Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro
 140 145 150
 Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro
 155 160 165
 Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly
 170 175 180
 Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro
 185 190 195
 Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly
 200 205 210
 Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg
 215 220 225
 Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln
 230 235 240
 Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp
 245 250 255
 Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly
 260 265 270
 His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe
 275 280 285
 Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile
 290 295 300
 Leu Gly Leu Arg Lys Glu Phe Glu Glu Ala Arg Lys Trp Val Ser
 305 310 315
 Lys Lys Leu His Phe Glu Lys Asp Val Asp Val Asn Leu Phe Glu
 320 325 330
 Ser Thr Ile Arg Ile Leu Gly Gly Leu Leu Ser Ala Tyr His Leu
 335 340 345
 Ser Gly Asp Ser Leu Phe Leu Arg Lys Ala Glu Asp Phe Gly Asn
 350 355 360
 Arg Leu Met Pro Ala Phe Arg Thr Pro Ser Lys Ile Pro Tyr Ser
 365 370 375
 Asp Val Asn Ile Gly Thr Gly Val Ala His Pro Pro Arg Trp Thr
 380 385 390
 Ser Asp Ser Thr Val Ala Glu Val Thr Ser Ile Gln Leu Glu Phe

395	400	405
Arg Glu Leu Ser Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala		
410	415	420
Val Glu Lys Val Thr Gln His Ile His Gly Leu Ser Gly Lys Lys		
425	430	435
Asp Gly Leu Val Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe		
440	445	450
Thr His Leu Gly Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr		
455	460	465
Tyr Glu Tyr Leu Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu		
470	475	480
Thr Gln Leu Leu Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg		
485	490	495
Thr His Leu Leu Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val		
500	505	510
Gly Glu Leu Ala His Gly Arg Phe Ser Ala Lys Met Asp His Leu		
515	520	525
Val Cys Phe Leu Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly		
530	535	540
Leu Pro Ala Ser His Met Glu Leu Ala Gln Glu Leu Met Glu Thr		
545	550	555
Cys Tyr Gln Met Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu		
560	565	570
Ile Val His Phe Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val		
575	580	585
Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr		
590	595	600
Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys		
605	610	615
Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe		
620	625	630
Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln		
635	640	645
Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe		
650	655	660
Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp		
665	670	675
Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala		
680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaaggctgtg tccaggtcct tcagttagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
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gcgcagctgc cctgggagga cggcaggatcc gggttgtct ccggcggcct 150
ccctcgaaag tggccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

ESTABLISHED

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ctggtcttcg tgccccacat gcgcgcgttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
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tgaacaggac aacctctcat caccggaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
<211> 327
<212> PRT
<213> Homo sapiens

<220>

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25, 65-71, 247-253, 285-291, 303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17

Met	Phe	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln	Leu	Pro	Trp	Glu	Asp	1	5	10	15
Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	Arg	Lys	Cys	Ser	20	25		30
Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	Phe	Phe	Ser	35	40		45
Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala	50	55		60
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys	65	70		75
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp	80	85		90
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe	95	100		105
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser	110	115		120
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp	125	130		135
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu				

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Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp		
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala		
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His		
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His		
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly		
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu		
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe		
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg		
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly		
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu		
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp		
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser		
320	325	

<210> 18
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 18
gcaaacgctt cgaggagtcc tgg 23

<210> 19
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

ESTATE

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<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
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gactggtcgg tgcccagaaa gtcttctcg ccactgacgc ccccatcagg 150
gattgggcct tctttcccccc ttcccttctg tgtctcctgc ctcatcggcc 200
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ggctaggggg gctgccttat ttaaagtggt tgtttatgat tcttatacta 350
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taaacagttt aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18
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<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ggctccgggg cgccccgcta ggccagtgcg ccgcccgtcg cccgcaggc 200
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cggtcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
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HUMAN GENOME

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caggagctgt tgacatgcga ccctccgctt gaattgccgt ctttctacat 950
gactccatct catcgccaag ttgtgtttga aggagacagc cttccttcc 1000
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<212> PRT
<213> Homo sapiens

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<222> 1-33
<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

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35 40 45
Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
50 55 60
Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
65 70 75
Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser
 95 100 105
 Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile
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 Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp
 125 130 135
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 140 145 150
 Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe
 155 160 165
 Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg
 170 175 180
 Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile
 185 190 195
 Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg
 200 205 210
 Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val
 215 220 225
 Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu
 230 235 240
 Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe
 245 250 255
 Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp
 260 265 270
 Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu
 275 280 285
 Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
 290 295 300
 Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln
 305 310 315
 Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg
 320 325 330
 Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser
 335 340 345
 Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp
 350 355 360
 Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln
 365 370 375
 Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro

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Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe 395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val 410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr 425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu 440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu 455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys 470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu 485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala 500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg 515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile 530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met 545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly 560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys 575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu 590	595	600
Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr 605	610	615
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 <222> 1-24

<223> Synthetic construct

<400> 25
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<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

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<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

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<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

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<212> PRT
<213> Homo sapiens

<220>
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<222> 1-21
<223> Signal peptide.

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Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
35 40 45
Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
50 55 60
Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
65 70 75
Lys Gly Ser Gln Lys Ser
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<210> 30
<211> 2128
<212> DNA
<213> Homo sapiens

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HUMAN
GENOME
PROJECT

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<211> 322
<212> PRT
<213> Homo sapiens

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Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
50 55 60
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
65 70 75
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
80 85 90
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
95 100 105
Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
110 115 120
Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
125 130 135
His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
140 145 150
Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
155 160 165
Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
170 175 180
Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
185 190 195
Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
200 205 210

Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu
				215					220					225
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu
				230					235					240
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu
				245				250						255
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln
				260				265						270
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr
				275				280						285
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr
				290				295						300
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala
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His	Leu	Val	Phe	Val	Lys	Val								
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<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

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<211> 335
<212> PRT
<213> Homo sapiens

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35 40 45
His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
50 55 60
Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
65 70 75
Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
80 85 90
Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
95 100 105
Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
110 115 120
Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
125 130 135
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
185 190 195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
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215 220 225
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260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

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290 295 300

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Glu Pro Glu Glu Gln
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<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
tgtccttgt cccagacttc tgtcc 25

<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
ctggatgcta atgtgtccag taaatgatcc ccttatcccc tcgcgatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25
<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
ggagatcgct gcgcgtggcca ggtcctccct gcatggtat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084
<212> DNA
<213> Homo sapiens

<400> 40
ggttcctggg cgctctgtta cacaagcaag atacagccag ccccacctaa 50
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tgatatttca gttcctgatt gtaaataacct cctaaggctg aagcttctgt 200
tactagccat tgtgagcttc agtttcttca tctgcaaaaat gggcataata 250
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aataccaaag aagcctacaa tggtggcatt agccaaaatt ctgttgattt 350
caacgttgtt ttattcactt ctatcgaaaa gccatggaaa agaaaatcaa 400
gacataaaaca caacacagaa cattgcagaa gttttaaaa caatggaaaa 450
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500
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ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
1 5 10 15
Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
20 25 30
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu
200 205 210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
230 235 240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
245 250 255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
260 265 270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu
275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
290 295 300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu
305 310 315

Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu
320 325 330

Arg Thr Ser Val

<210> 42
<211> 1594
<212> DNA
<213> Homo sapiens

<400> 42
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cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
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tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350
ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400
tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
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ccctataata aattttactc tataaaaaaa aaaaaaaaaa aaaa 1594

<210> 43
<211> 263
<212> PRT
<213> Homo sapiens

<400> 43
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
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Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
20 25 30
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly	Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys		
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu		
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp		
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp		
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr		
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu		
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe		
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val		
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn		
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe		
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala		
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile		
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
ggagaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgagtc tgcaac 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
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attccggcct gaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1950
aaaaaaaaaaa aaaaaaaaga 1969

<210> 50
<211> 283
<212> PRT
<213> Homo sapiens

<400> 50
Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu
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Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
20 25 30
Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
35 40 45
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
50 55 60
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
65 70 75
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
80 85 90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
95 100 105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
110 115 120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
125 130 135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
140 145 150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr
														180
170									175					
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
														195
185									190					
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
														210
200									205					
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
														225
215									220					
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
														240
230									235					
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
														255
245									250					
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
														270
260									265					
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val		
275									280					

<210> 51

<211> 1734

<212> DNA

<213> Homo sapiens

<400> 51

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<210> 52
<211> 440
<212> PRT
<213> Homo sapiens

<400> 52
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Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
20 25 30
Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
35 40 45
Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50	55	60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr		
65	70	75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly		
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala		
95	100	105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val		
110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val		
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile		
140	145	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro		
155	160	165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser		
170	175	180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln		
185	190	195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly		
200	205	210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln		
215	220	225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly		
230	235	240
Ser Ser Asn Ser Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser Ser		
245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly		
260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser		
275	280	285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser		
290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly		
305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Asn Gly His		
320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly		
335	340	345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
350 355 360

Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
365 370 375

Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
380 385 390

Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
395 400 405

Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
410 415 420

Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
425 430 435

Ser Ser Arg Ile Pro
440

<210> 53

<211> 3580

<212> DNA

<213> Homo sapiens

<400> 53

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Homo sapiens

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<211> 280

<212> PRT

<213> Homo sapiens

<400> 54
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 His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr
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 Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser
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<212> DNA
<213> Homo sapiens

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<210> 56
<211> 299
<212> PRT
<213> Homo sapiens

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<211> 4277

<212> DNA

<213> Homo sapiens

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<210> 58

<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys
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His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val
					155				160				165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met
					170				175				180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu
					185				190				195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val
					200				205				210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr
					215				220				225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile
					230				235				240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser
					245				250				255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser
					260				265				270	

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu
 275 280 285
 Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met
 290 295 300
 Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr
 305 310 315
 Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser
 320 325 330
 Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu
 335 340 345
 Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala
 350 355 360
 Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala
 365 370 375
 Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln
 380 385 390
 Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln
 395 400 405
 Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp
 410 415 420
 Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu
 425 430 435
 Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg
 440 445 450
 Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu
 455 460 465
 Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser
 470 475 480
 Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro
 485 490 495
 Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
 500 505 510
 Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
 515 520 525
 Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
 530 535 540
 Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
 545 550 555
 Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys	Glu Gln Gln Ile Gln	
575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser	Ser Ser Gln Pro Asp	
590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro	Asp Arg Pro Thr Ile	
605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val	Thr Trp Ile Pro Arg	
620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr Lys	
635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala Ile	
650	655	660
Pro Pro Ser Arg Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys Gly	
665	670	675
Thr Ser Tyr Lys Phe Arg Val Arg Ala	Leu Asn Met Leu Gly Glu	
680	685	690
Ser Glu Pro Ser Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly Tyr	
695	700	705
Ser Gly Arg Val Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile Thr	
710	715	720
Phe Thr Asp Ala Val Asn Glu Thr Thr	Ile Met Leu Lys Trp Met	
725	730	735
Tyr Ile Pro Ala Ser Asn Asn Asn Thr	Pro Ile His Gly Phe Tyr	
740	745	750
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr Lys	
755	760	765
Lys Asp Met Val Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser His	
770	775	780
Leu Gln Pro Glu Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe Asn	
785	790	795
Glu Gly Gly Glu Ser Glu Phe Ser Asn	Val Met Ile Cys Glu Thr	
800	805	810
Lys Ala Arg Lys Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro Pro	
815	820	825
Thr Leu Ala Pro Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu Arg	
830	835	840
Pro Val Gly Thr Gly Ala Met Val Ala	Arg Ser Ser Asp Leu Pro	
845	850	855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
 860 870
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 875 880 885
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
 890 895 900
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
 905 910 915
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
 920 925 930
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
 935 940 945
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
 950 955 960
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
 965 970 975
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
 980 985 990
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
 995 1000 1005
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
 1010 1015 1020
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
 1025 1030 1035
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
 1040 1045 1050
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
 1055 1060 1065
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
 1070 1075 1080
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
 1085 1090 1095
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
 1100 1105 1110
 Pro Pro Leu Thr Ile
 1115

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

卷之三

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 59
ggaaacaca gcagtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgttag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
cccccaag ccaggatccg gtacagcgta aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
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cacggccgc gagggttccc gcgcgctcag ccggcggtat ctgcggcg 150
tgctgctcct gctactgctg ctgctgctgc ggcagccgt aaccgcgcg 200
gagaccacgc cggcgcccc cagagccctc tccacgctgg gctcccc 250
cctcttacc acgccgggtg tccccagcgc cctcactacc ccaggcctca 300
ctacgccagg cacccccaaa accctggacc ttccgggtcg cqgcqcaqqcc 350

ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
cctgagacag cgttacaaga atgtgcttca ghatgttaac ctgcgaaatt 450
tcagccatgg tcagaccaggc ctggacaggc ttagagacgg cctcggtgg 500
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gccccctctc ctatgttca cacaaggata tgctgagaat aaacatgtta 1650
cacatggaaa a 1661

<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63
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Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg
 20 25 30

Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala
 35 40 45

Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
 50 55 60

Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro
 65 70 75

Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser
 80 85 90

Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg
 95 100 105

Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe
 110 115 120

Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val
 125 130 135

Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp
 140 145 150

Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His
 155 160 165

Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala
 170 175 180

Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val
 185 190 195

Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser
 200 205 210

Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys
 215 220 225

Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met
 230 235 240

Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val
 245 250 255

Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 64

ccttcacccgt cagtacacca tggc 25
<210> 65
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 65
gtcacacaca gctctggcag ctgag 25

<210> 66
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 66
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<210> 67
<211> 1564
<212> DNA
<213> Homo sapiens

<400> 67
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aacacccaca gatccctcta tgactgcaat gtgaggtgtc cggcttgct 100
ggcccgacaa gcctgataag catgaagctc ttatcttgg tggctgttgt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccacccata gaaacatcag tggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
gcccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
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tccctcgcccc gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaaag acagtcttcg 650
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ttttatttct ctca 1564

<210> 68
<211> 183
<212> PRT
<213> Homo sapiens

<400> 68
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20 25 30
Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
35 40 45
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu
				65					70					75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val
				80					85					90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr
				95					100					105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp
				110					115					120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala
				125					130					135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
				140					145					150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys
				155					160					165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys
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Met	Leu	Ser												

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
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 tccctttgca ttccccacccc tccgggcttt gcgtcttccct ggggacccccc 200
 tcgcgggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250
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BIOINFORMATICS

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<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20				25				30		
Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35				40				45		

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
 50 55 60
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
 65 70 75
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
 80 85 90
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
 95 100 105
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
 110 115 120
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
 125 130 135
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
 140 145 150
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
 155 160 165
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
 170 175 180
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
 185 190 195
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
 200 205 210
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
 215 220 225
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 230 235 240
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
 245 250 255
 Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
 tctcaatctg ctgacacctcg gatccgcctg accttgtaat ccacccatcc 50
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 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatttt catgttagtat tttctaagtt 250
atattttagt aattcatatg ttttagatta taggaaaa catacttg 300
aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
ggatttgttc ttttatcccc cttaaagt catccgtcct tggctcagga 400
tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
gtacacagca gaatagtaca agtcacccta caactactac ttcttggac 550
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ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctggca acatggtaa actctgtc tactaaaata cggaaaaacta 1700
gccgggtgtg gtggcgccgc gtgcctgtaa tcccagctac ttgggaggct 1750
gaggcacaag aatcgcttga gccagttgg gctacaaagt gagactccgt 1800
ctgaaaaga 1809

<210> 72

<211> 363

<212> PRT

<213> Homo sapiens

<400> 72

Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile
1 5 10 15

Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
20 25 30

Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45

Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60

Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75

Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90

Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105

Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120

Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135

Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150

Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165

Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180

Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195

Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210

Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys
230 235 240

Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala
245 250 255

Val Gln Asn Ser Thr Tyr Thr Ser Val Ile Thr Ser Cys Ser
260 265 270

Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser
275 280 285

Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln
290 295 300

Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn
305 310 315

Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr
320 325 330

Ser Ser Lys Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg
335 340 345

Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp
350 355 360

Leu Ile Arg

<210> 73
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 73
aattcatggc aaatatttcc cttccc 26

<210> 74
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 74
tggtaaactg gcccaaactc gg 22

<210> 75
<211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcat ccgtccttgg ctcaggattt ggagagcttg caccaccaaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
gccgagtgaaa acaaaggctg gggctggcg gggccatgg cgctgccatc 50
ccgaatcctg ctggaaac ttgtgtttct gcagagctct gctgttctcc 100
tgcactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
caccatcaact actgccaccc ttagagac ctggccgtcc gcctggaggt 200
caccgacggc ccccccggcca ccccccgccta ctgggacggc gagaaggagg 250
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ccactctcag caccccacat ttgcatctgc tggtgaccc gccaaccatca 1950
caataaaagtc cccatctgat tttaaaaaaaa aaaaaaaaaa 1989

<210> 77
<211> 341
<212> PRT
<213> Homo sapiens

<400> 77
Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu
1 5 10 15
Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
 80 85 90
 Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
 95 100 105
 Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
 110 115 120
 Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
 125 130 135
 Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu
 140 145 150
 Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp
 155 160 165
 Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu
 170 175 180
 His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala
 185 190 195
 Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser
 200 205 210
 Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val
 215 220 225
 Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln
 230 235 240
 Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu
 245 250 255
 Val Thr Val Leu Leu Ala Ala Arg Arg Arg Gly Gly Tyr Glu
 260 265 270
 Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn
 275 280 285
 Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
 290 295 300
 Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
 305 310 315
 Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
 320 325 330
 Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
 335 340

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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cagtctccga gctgaccagg aggactgct tgagaagctg ctggaccgcc 150
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cactgccaag gagtaactgga tgttcaaact cccgcaactcc tccagcccag 300
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gccattgggtt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
1 5 10 15

Thr Tyr Gly Thr Thr Ser Ser Leu Arg Ala Asp Gln Glu Ala
20 25 30

Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45

Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60

Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75

Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90

Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
 110 115 120
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
 125 130 135
 Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
 140 145 150
 Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
 155 160 165
 Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
 170 175 180
 Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met
 185 190 195
 Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr
 200 205 210
 Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp
 215 220 225
 Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
 230 235 240
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu
 245 250 255
 Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe
 260 265 270
 Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser
 275 280 285
 Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro
 290 295 300
 Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val
 305 310 315
 Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile
 320 325 330
 Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe
 335 340 345
 Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu
 350 355 360
 Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn
 365 370 375
 Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile
 380 385 390
 Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser		
410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu		
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly		
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser		
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu Ile		
470	475	

<210> 80
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 80
tttgcggtc accattgtct gc 22

<210> 81
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 81
cgttaggtgac acagaagccc agg 23

<210> 82
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-49
<223> Synthetic construct.

<400> 82
tacggcatga ccggctcctt tcctatgagg aactccagg cactgatat 49

<210> 83
<211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

gacagtggag ggcagtggag aggaccgcgc tgtcctgctg tcaccaagag 50
ctggagacac catctccac cgagagtcat ggccccattg gccctgcacc 100
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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
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ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750
aaaacacgac ccacacgagg acctcgatt aaagtatttt cgaaaaaaa 1800
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu
1 5 10 15

Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln
20 25 30

Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
35 40 45

Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
50 55 60

Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
65 70 75

Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
80 85 90

Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
95 100 105

Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
110 115 120

His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
125 130 135

Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
140 145 150

Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
155 160 165

Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
 170 175 180
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
 185 190 195
 Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr
 200 205 210
 Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala
 215 220 225
 Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr
 230 235 240
 Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp
 245 250 255
 Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro
 260 265 270
 Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala
 275 280 285
 Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln
 290 295 300
 Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala
 305 310 315
 Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile
 320 325 330
 Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg
 335 340 345
 Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg
 350 355 360
 Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn
 365 370 375
 Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu
 380 385 390
 Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala
 395 400 405
 Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu
 410 415 420
 Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp
 425 430 435
 Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser
 440 445 450
 Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85
<211> 3316
<212> DNA
<213> Homo sapiens

<400> 85
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gaactcagag ccggaaagcc cccattcaact agaagcactg agagatgcgg 200
ccccctcgca gggtctgaat ttccctgctgc tgttcacaaa gatgcttttt 250
atcttaact ttttgttttc cccacttccg acccccggcgt tgatctgcat 300
cctgacattt ggagctgcca tcttcttgac gctgatcacc agacctaacc 350
ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggaa 400
ggagcacgga agggggtttc ccagaagaac aatgaccaa caagttgctg 450
cttctcagat gccaagacta tgtatgaggt tttccaaaga ggactcgctg 500
tgtctgacaa tggccctgc ttggatata gaaaacccaaa ccagccctac 550
agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600
ctgtctcttg cataaagggtt ataaatcatc accagaccag tttgtcggca 650
tctttgctca gaataggcca gagtggatca tctccgaatt ggcttggtac 700
acgtactcta tggtagctgt acctctgtat gacaccttgg gaccagaagc 750

Nucleotide sequence

catcgatcat attgtcaaca aggctgatat cgccatggtg atctgtgaca 800
caccccaaaa ggcattggtg ctgataggaa atgtagagaa aggcttcacc 850
ccgagcctga aggtgatcat ccttatggac cccttgcgt atgacctgaa 900
gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgctg 950
agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000
gacctgagcg tcatactgctt caccagtgg accacaggtg accccaaagg 1050
agccatgata acccatcaaa atattgttcc aaatgctgct gccttctca 1100
aatgtgtgga gcatgcttat gagcccactc ctgatgatgt ggccatatcc 1150
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cagctgtgga gccagagttg gattctcca agggatatt cggttgctgg 1250
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cagtaggaac tggggagtaa atctgttccc tacagttgc tgctgagctg 3050
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aactgatctc ccccaccctt ggatttaggt tcctgctcta cttacccac 3250
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tattacagat aaaaaa 3316

<210> 86
<211> 739
<212> PRT
<213> Homo sapiens

<400> 86
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Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
20 25 30

Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser
 35 40 45
 Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile
 50 55 60
 Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys
 65 70 75
 Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg
 80 85 90
 Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val
 95 100 105
 Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
 110 115 120
 Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu
 125 130 135
 Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu
 140 145 150
 Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys
 155 160 165
 Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His
 170 175 180
 Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala
 185 190 195
 Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr
 200 205 210
 Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu
 215 220 225
 Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile
 230 235 240
 Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu
 245 250 255
 Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro
 260 265 270
 Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu
 275 280 285
 Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe
 290 295 300
 Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys
 305 310 315
 Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr

320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala		
335	340	345
Ala Phe Leu Lys Cys Val		
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp		
350	355	360
Val Ala Ile Ser Tyr		
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val		
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg		
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro		
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn		
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val		
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp		
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu		
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser		
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val		
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe		
500	505	510
Leu		
Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu		
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr		
530	535	540
Leu		
Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn		
545	550	555
Ala		
Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala		
560	565	570
Trp		
Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp		
575	580	585
Ile		
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile		
590	595	600
Glu		
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu		
605	610	615

Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His
620 625 630

Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp
635 640 645

Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly
650 655 660

Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile
665 670 675

Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr
680 685 690

Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser
695 700 705

Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly
710 715 720

Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu
725 730 735

His Ile Gln Asp

<210> 87
<211> 2725
<212> DNA
<213> Homo sapiens

<400> 87
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gccccggcg ggcccggggc ccctaagcca ttccctgaagt catggctgg 100
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cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200
ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
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atcctggaca ctcggcgagc catcagtgaa gccaatgaag acccagagcc 350
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gacacagagc tgaaccgtcg ccgccggcgc ttctgcagca aagttgaggg 950
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aaaaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88
<211> 660
<212> PRT
<213> Homo sapiens

<400> 88
Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala
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Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr
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Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
35 40 45
Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
50 55 60
Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
65 70 75
Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
80 85 90
Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
95 100 105
Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
110 115 120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp
 140 145 150

 Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn
 155 160 165

 Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu
 170 175 180

 Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser
 185 190 195

 Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp
 200 205 210

 Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His
 215 220 225

 Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu
 230 235 240

 Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His
 245 250 255

 Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser
 260 265 270

 Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr
 275 280 285

 Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu
 290 295 300

 Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu
 305 310 315

 Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro
 320 325 330

 Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met
 335 340 345

 Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro
 350 355 360

 Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser
 365 370 375

 Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val
 380 385 390

 Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe
 395 400 405

 Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr
 410 415 420

 Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly		
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys		
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg		
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val		
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu		
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr		
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp		
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu		
635	640	645
Pro Pro Pro Lys Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr		
650	655	660

<210> 89
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgttg acacg 25
<210> 90
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 90
cctcaaccag gccacgggcc ac 22

<210> 91
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 91
cccaggcaga gatgcagtagc aggc 24

<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 92
cctccagtag gtggatggat tggctc 26

<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
ctcacccat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

<400> 94

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ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgGGat 200
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tcatgttgct ggtggaccag attggtaact cccatgtgca ttctactgac 550
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THE COUNCIL OF THE STATE

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<211> 307
<212> PRT
<213> Homo sapiens

<400> 95
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Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
35 40 45
Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
50 55 60
Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
65 70 75
Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
80 85 90
Val Val His Glu His Ser His Asp His Thr Gln Leu His
95 100 105
Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
110 115 120
Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
125 130 135
Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
140 145 150
Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
155 160 165
Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
170 175 180
Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
185 190 195
Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
200 205 210
Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
215 220 225
Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

230 235 240

Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu
245 250 255

Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly
260 265 270

His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg
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Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile
290 295 300

Leu Ser Val Gly His Gln His
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<212> DNA
<213> Artificial

<220>
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<222> 1-25
<223> Synthetic construct.

<400> 96
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<210> 97
<211> 25
<212> DNA
<213> Artificial

<220>
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<223> Synthetic construct.

<400> 97
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<210> 98
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct.

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<210> 99
<211> 1429

<212> DNA
<213> Homo sapiens

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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					20				25				30	

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
					35				40				45	

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
					50				55				60	

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
					65				70				75	

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
					80			85					90	

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
					95				100				105	

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
					110				115				120	

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
					125				130				135	

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
					140			145					150	

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
					155				160				165	

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
					170				175				180	

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
					185				190				195	

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
					200			205					210	

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
					215				220				225	

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
					230				235				240	

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr
 245 250 255
 Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu
 260 265 270
 Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val
 275 280 285
 Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro
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 Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met
 305 310 315
 Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu
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 Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu
 335 340 345
 Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser
 350 355 360
 Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile
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<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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					20				25						30
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	
					35				40						45
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	
				50					55						60
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	
					65				70						75
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	
					80				85						90
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	
					95				100						105
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	
				110					115						120
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	
				125					130						135
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	
				140					145						150
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	
				155					160						165
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
				170					175						180
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	
				185					190						195
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	

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215	220	225	
Val Leu Ile Ala His Phe Leu Gly Val Asp His Cys Gly His Lys			
230	235	240	
His Gly Pro His His Pro Glu Met Ala Lys Lys Leu Ser Gln Met			
245	250	255	
Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr			
260	265	270	
Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp			
275	280	285	
His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu			
290	295	300	
Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro			
305	310	315	
Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu			
320	325	330	
Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala			
335	340	345	
Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala			
350	355	360	
Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser			
365	370	375	
Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala			
380	385	390	
Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala			
395	400	405	
Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr			
410	415	420	
Leu Pro Thr Val Ile Ala Glu Leu Gln Gln Phe Leu Arg Gly Ala			
425	430	435	
Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg			
440	445	450	
Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys			
455	460	465	
Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys			
470	475	480	
Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile			
485	490	495	

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 Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe
 515 520 525
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 Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val
 575 580 585
 Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu
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 Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg
 605 610 615
 His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu
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 Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr
 635 640 645
 Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met
 650 655 660
 Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala
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 680 685 690
 Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg
 695 700 705
 Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala
 710 715 720
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 725 730 735
 Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu
 740 745 750
 Ala Ala Ser Gly Leu Ala Leu Leu Trp Lys Pro Val Thr Val
 755 760 765
 Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu
 770 775 780
 Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr

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Val Val Pro Gln Ile Tyr Arg His Met Gln	Glu Glu Phe Arg Gly	
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Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala		
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu		
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile		
845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu		
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe		
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr		
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile		
905	910	915
His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser		
920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala		
935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp		
950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro		
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val Arg Pro Glu Glu Glu		
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe		
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu		
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg		
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe		
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly		
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe		
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Arg Gln Leu Phe Leu Ala Gln Gln Arg
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<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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ttcaaggagt taaagttact tacactgtgc agtatttcat cacaattgg 200
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atgtttgcc catatctatt accgtgttcc tttttctgt gatggctat 600
tccatctacc gatatatcca cggtggcaaa gagaaacacc cagcaaattt 650
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<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

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				20					25				30	
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40				45	
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55				60	
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70				75	
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85				90	
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95					100				105	
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110					115				120	
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130				135	
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145				150	
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160				165	

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile
 170 175 180
 Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys
 185 190 195
 Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys
 200 205 210
 Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val
 215 220 225
 Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro
 230 235 240
 Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu
 245 250 255
 Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser
 260 265 270
 Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys
 275 280 285
 Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys
 290 295 300
 Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser
 305 310 315
 Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu
 320 325 330
 Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp
 335 340 345
 Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro
 350 355 360
 Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr
 365 370 375
 Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
 380 385 390
 Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
 395 400 405
 Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
 410 415 420
 Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
 425 430 435
 Leu Tyr Val Gln Met Glu Asn
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<210> 105

ARTIFICIAL DNA SEQUENCES

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<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
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<210> 106
<211> 18
<212> DNA
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<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
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<210> 107
<211> 18
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<222> 1-18
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<400> 107
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<210> 108
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<400> 108
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<222> 1-51

<223> Synthetic construct.

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<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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tctgctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150

gctcctgggg ggcccagatc atcgggggcc acgaggtgac ccccaactcc 200

aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250

cttcctgctg cgagcccgct ggggtgtctc ggccgcccac tgcttcagcc 300

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gccgctccag gcctggaatg ttccgtggct gggccccacg ggaaggctga 1000

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tgcaaaggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

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Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp	
				20				25					30		
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg	
				35				40					45		
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly	
				50				55					60		
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys	
				65				70					75		
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala	
				80				85					90		
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile	
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Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala	
				110				115					120		
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly	
				125				130					135		
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro	
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Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val	
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Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val	
				170				175					180		
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His	
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Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg	
				200				205					210		
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg	
				215				220					225		
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly	
				230				235					240		
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val	
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Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagtcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
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<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

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<222> 1-44
<223> Synthetic construct.

<400> 114
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<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
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<210> 116
<211> 331
<212> PRT
<213> Homo sapiens

<400> 116
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Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
35 40 45
Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
50 55 60
Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
65 70 75
Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
80 85 90
Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
95 100 105
Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Arg Val Asp Ile
110 115 120
Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
125 130 135
Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
140 145 150
Phe Leu Leu Thr Asn Leu Leu Asp Lys Leu Lys Ala Ser Ala
155 160 165
Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
170 175 180
His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
185 190 195
Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
200 205 210
Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
215 220 225

Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His
230 235 240

Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro
245 250 255

Ile Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro
260 265 270

Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly
275 280 285

Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala
290 295 300

Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg
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Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln Pro Leu Pro
320 325 330

Arg

<210> 117
<211> 2249
<212> DNA
<213> Homo sapiens

<400> 117
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<210> 118
<211> 544
<212> PRT
<213> Homo sapiens

<400> 118
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20 25 30
Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45
Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60
Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75
His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90
Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105
Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120
Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135
Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150
Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165
Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180
Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195
Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210
Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225
Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu
 245 250 255
 Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr
 260 265 270
 Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala
 275 280 285
 Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr
 290 295 300
 Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr
 305 310 315
 Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala
 320 325 330
 Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu
 335 340 345
 Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala
 350 355 360
 Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val
 365 370 375
 Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser
 380 385 390
 Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr
 395 400 405
 Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro
 410 415 420
 Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly
 425 430 435
 His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro
 440 445 450
 Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile
 455 460 465
 Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr
 470 475 480
 Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
 485 490 495
 Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
 500 505 510
 Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
 515 520 525
 Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser

530

535

540

Ser Pro Glu Asp

<210> 119
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 119
cgggacagga gacccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 120
ggccaagtga tccaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-49
<223> Synthetic construct.

<400> 121
ctgcgggacc tgacttagatt ctacgacaag gtactttctt tgcatgggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122
gagatagggta gtctgggtt aagttcctgc tccatctcag gagcccctgc 50
tccccacccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagcccccc taacccgcgc ggggagcgcc caggatgccg 200

cgcgccccact cgaggccaggc ggcgtactgc gcgcgcttct cttacacctg 250
gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300
ccctggtcct gtctgtgggc atctatgcag aggttgcgcg gcagaaatat 350
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatttcct 400
gggcgtcgcc atgttcatgg tctcattcat tggtgtgctg gcgtccctcc 450
gtgacaacctt gtaccttctc caagcattca tgtacatcct tggatctgc 500
ctcatcatgg agtcattgg tggcggtgg gccttgacct tccggAACCA 550
gaccatttgc ttccctgaacg acaacattcg aagaggaatt gagaactact 600
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
aagtgcgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700
cgactgcagt gcccctggac ccctggcctg tgggtgccc tacacctgct 750
gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
atcgacaagg agcgtttcag tgtgcaggat gtcatctacg tgcggggctg 850
caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
gcatcctcct gggcatcctg cttccccagt tcctgggggt gctgctgacg 950
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ctcttctcag cctccctagg gccttgagcc ctcttgcaag ggcggctgct 1600
tccttgagcc tagtttttt ttacgtgatt tttgttaacat tcatttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttcccccgcatt 1700
gtcttattct tgcccttccc ccaaccagtt tgttaatcaa acaataaaaa 1750
catgtttgt tttgtttta aaaaaaaaa 1778

<210> 123
<211> 294
<212> PRT
<213> Homo sapiens

<400> 123
Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe
1 5 10 15
Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
20 25 30
Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
35 40 45
Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
50 55 60
Ala Pro Ala Ile Ile Leu Ile Leu Gly Val Val Met Phe Met
65 70 75
Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
80 85 90
Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
95 100 105
Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
110 115 120
Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
125 130 135
Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
140 145 150
Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
155 160 165
Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
170 175 180
Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
185 190 195
Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
200 205 210
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
215 220 225
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

230 235 240

Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr
245 250 255

Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Val Thr Asp
260 265 270

Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly
275 280 285

Thr Gly Cys Cys Leu Cys Tyr Pro Asn
290

<210> 124
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 124
atcatctatt ccaccgtggtt ctggc 25

<210> 125
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 125
gacagagtgc tccatgtatga tgtcc 25

<210> 126
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 126
cctgtctgtg ggcatctatg cagaggtaa gcggcagaaa tataaaaccc 50

<210> 127
<211> 1636
<212> DNA
<213> Homo sapiens

<400> 127
gaggagcggg ccgaggactc cagcgtgcc aggtctggca tcctgcactt 50
gctgccctct gacacctggg aagatggccg gcccgtggac ctccaccctt 100
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtcccac 150
tgcagttctc atcctcgccc caaaagtcat caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gcccgtgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tggcagcct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggc atcacagcta 350
acatcctcca gctgcaggtg aagccctcg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtaa 450
gaccatcgtg gagttccaca tgacgactga ggcccaagcc accatccgca 500
tggacaccag tgcaagtggc cccacccgccc tggcctcag tgactgtgcc 550
accagccatg ggagcctgctg catccaactg ctgtataagc tctccttcct 600
ggtaaacgccc ttagctaagc aggtcatgaa cctccttagtgc ccatccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccc tgatcgagggc ttccttcaat 700
ggcatgtatg cagacctct gcagctggtg aaggtgccc ttccctcag 750
cattgaccgt ctggagtttgc accttctgtt tcctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaagttgt tggactcaca gggaaagggtg 850
accaagtggc tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccg ttcaagcctca tcgtgagtc ggacgtggtg aaagctgcag 950
tggctgctgt gctctctcca gaagaattca tggcctgtt ggactctgtg 1000
cttcctgaga gtgcccacatcg gctgaagtca agcatcgggc tgatcaatga 1050
aaaggctgca gataagctgg gatctaccca gatcgtgaag atcctaactc 1100
aggacactcc cgagttttt atagaccaag gccatgccaa ggtggcccaa 1150
ctgatcgtgc tggaaagtgtt tccctccagt gaagccctcc gcccttgtt 1200
caccctgggc atcgaagcca gctcggaaagc tcagtttac accaaagggtg 1250
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
gatctggggtt cccagtgtca ttggtaagg ccttgggattt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttgc cttactccag ctccttgc 1500
gaaaccgc tccctgtct cccagtgaag acttggatgg cagccatcag 1550
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
cctctctgca atcaataaac acttgccgt gaaaaa 1636

<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
1				5				10						15
Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
				20				25						30
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
				35				40						45
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
				50				55						60
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
				65				70						75
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
				80				85						90
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
				95				100						105
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
				110				115						120
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
				125				130						135
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
				140				145						150
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
				155				160						165
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu
				170				175						180
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu
				185				190						195
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly
				200				205						210
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu
				215				220						225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
 230 235 240
 Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
 245 250 255
 Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
 260 265 270
 Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
 275 280 285
 Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
 290 295 300
 Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
 305 310 315
 Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
 320 325 330
 Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
 335 340 345
 Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
 350 355 360
 Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
 365 370 375
 Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
 380 385 390
 Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
 395 400 405
 Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
 410 415 420
 Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
 425 430 435
 Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
 440 445 450
 Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
 455 460 465
 Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
 470 475 480
 Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129
gagcgaacat ggcagcgcgt tggcggttt ggtgtgttc tgtgaccatg 50
gtggtggcgc tgctcatcgt ttgcacgtt ccctcagcct ctgccaaag 100
aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atgaaatgga 150
ctaacaaaag acctgtata agaatgaatg gagacaagtt ccgtcgccct 200
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcactgctct 250
ccaactgcat agacagtgtg tcgttgcaa gcaagctgat gaagaattcc 300
agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350
tttttgcca tggtgattt ttagtgcaggc tctgatgtat ttcagatgct 400
aaacatgaat tcagctccaa ctccatcaa ctccctgca aaaggaaac 450
ccaaacgggg tgatacatat gagttacagg tgcggggttt ttcagctgag 500
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550
tagaccccca aattatgctg gtcccttat gttggattt ctggctg 600
ttattggtg acttgtgtat cttcgaagaa gtaatatgga atttctctt 650
aataaaaactg gatggcctt tgcaagttt tggttgc ttgctatgac 700
atctggtcaa atgtggAACC atataagagg accaccatat gcccataaga 750
atccccacac gggacatgtg aattatatcc atgaaagcag tcaagcccag 800
ttttagctg aaacacacat tgccctctg ttatggtg gagttacatt 850
aggaatggtg ctttatgtg aagctgctac ctctgacatg gatattggaa 900
agcgaaagat aatgtgtgtg gctggattt gacttgttattt attattcttc 950
agttggatgc tctctatttt tagatctaaa tatcatggct acccatacag 1000
ctttctgatg agttaaaaag gtcccgaga tatatagaca ctggagttact 1050
ggaaattgaa aaacgaaaat cgtgtgttt tgaaaagaag aatgcaactt 1100
gtatattttt tattacctt tttttcaag tgatttaat agttaatcat 1150
ttaaccaaag aagatgtgtt gtgccttaac aagcaatcct ctgtcaaaat 1200
ctgaggtatt tgaaaataat tatcccttta accttctt cccagtgaac 1250
tttatggAACC atttaattttt gtacaattaa gtatattata aaaattgtaa 1300
aactactact ttgttttagt tagaacaaag ctcaaaacta ctttagttaa 1350
cttggcattc tgattttata ttgccttac caaagatggg gaaagtaagt 1400
cctgaccagg tgcccccaca tatgcctgtt acagataact acattaggaa 1450

ttcattctta gcttcttcat ctttgtgtgg atgtgtatac tttacgcac 1500
tttcctttg agtagagaaa ttatgtgtgt catgtggctc tctgaaaatg 1550
gaacaccatt cttagagca cacgtctagc cctcagcaag acagttgttt 1600
ctccctcctcc ttgcataattt cctactgcgc tccagcctga gtgatagagt 1650
gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataattct 1700
gcttgagttat ggtgttaact accttgcatt tagaaagatt tcagattcat 1750
tccatctcct tagtttctt ttaaggtgac ccatctgtga taaaaatata 1800
gcttagtgct aaaatcagtg taacttatac atggcctaaa atgttctac 1850
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cagttagaaa aggactccct ggccaggcgac agtgacttac gcctgtaatc 1950
tcagcacttt gggaggccaa ggcaggcaga tcacgaggc aggagttcga 2000
gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaaa 2050
attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100
tgaggcacga gaatcacttg aactcaggag atggaggcatt cagtgagccg 2150
agatcacgccc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200
aaaaaaaaaa aaa 2213

<210> 130
<211> 335
<212> PRT
<213> Homo sapiens

<400> 130
Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
1 5 10 15
Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
20 25 30
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
35 40 45
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
50 55 60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
65 70 75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
80 85 90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
95 100 105

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp
 110 115 120
 Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser
 125 130 135
 Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg
 140 145 150
 Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
 155 160 165
 Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
 170 175 180
 Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
 185 190 195
 Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
 200 205 210
 Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
 215 220 225
 Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
 230 235 240
 Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
 245 250 255
 Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
 260 265 270
 Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu
 275 280 285
 Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys
 290 295 300
 Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser
 305 310 315
 Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr
 320 325 330
 Ser Phe Leu Met Ser
 335

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
 aagcaaccaa actgcaagct ttgggagttt ttcgctgtcc ctgccctgct 50
 ctgcttaggga gagaacgcca gagggaggcg gctggcccg 100

tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
cttggcgctg gcggtaactgg ccccccggagc aggggagcag aggoggagag 200
cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250
aggtaacat ttcatccagg aagtcaaggta gtgaaacttc cttttatcaa 300
ctttatgaag acacgtggga cttccttct gaatgcctac acaaactctc 350
caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
ttaacagaat ctggaaataa tttaagggt ctagatccaa attataacaac 450
atggatggat gtcatggaga ggcattggcta ccgaacacag aaatttggga 500
aactggacta tacttcagga catcaactcca ttagtaatcg tgtggaagcg 550
tggacaagag atgttgctt cttactcaga caagaaggca ggcccatgg 600
taatcttatac cgtaacagga ctaaagtcaag tggatggaa agggattggc 650
agaatacaga caaaggcagta aactggtaa gaaaggaagc aattaattac 700
actgaaccat ttgttattta cttgggatta aatttaccac acccttaccc 750
ttcaccatct tctggagaaa atttggatc ttcaacattt cacacatctc 800
tttattggct tgaaaaagtgc tctcatgatg ccatcaaaat cccaaagtgg 850
tcaccttgt cagaaatgca ccctgttagat tattactctt cttatacaaa 900
aaactgcact ggaagattta caaaaaaaga aattaagaat attagagcat 950
tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000
ttggcccttc atcaattaga tcttcttcag aaaactattt tcataactc 1050
ctcagaccat ggagagctgg ccatggaaaca tcgacagttt tataaaatga 1100
gcatgtacga ggctagtgc a catgttccgc ttttgcgtat gggaccagga 1150
attaaagccg gcctacaagt atcaaatgtg gtttctttt tggatattta 1200
ccctaccatg cttgatattt ctggaaattcc tctgcctcag aacctgagtg 1250
gatactctt gttgccgtt tcatcagaaa catttaagaa tgaacataaa 1300
gtcaaaaacc tgcatccacc ctggattctg agtgaattcc atggatgtaa 1350
tgtgaatgcc tccacccata tgcttcgaac taaccactgg aaatatata 1400
cctattcgga tggtgcatca atattgcctc aactcttgc tcttcctcg 1450
gatccagatg aattaacaaa tggatgttgc aaatttccag aaattactta 1500
ttcttggat cagaagcttc attccattat aaactaccct aaagttctg 1550

ESTABLISHED

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<210> 132
<211> 536
<212> PRT
<213> Homo sapiens

<400> 132
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20 25 30
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
35 40 45
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
50 55 60
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
65 70 75

Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly
 80 85 90
 Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu
 95 100 105
 Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly
 110 115 120
 Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His
 125 130 135
 His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala
 140 145 150
 Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg
 155 160 165
 Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr
 170 175 180
 Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr
 185 190 195
 Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr
 200 205 210
 Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His
 215 220 225
 Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys
 230 235 240
 Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr
 245 250 255
 Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys
 260 265 270
 Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu
 275 280 285
 Thr Asp Ala Met Leu Gly Glu Ile Leu Ala Leu His Gln Leu
 290 295 300
 Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly
 305 310 315
 Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr
 320 325 330
 Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile
 335 340 345
 Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile
 350 355 360
 Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys 380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser 395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg 410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile 425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr 440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln 455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val 470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile 485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln 500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln 515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val 530	535	

<210> 133
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 133
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ctacatccta ggccttctgg ggctttggg cacactggtt gccatgctgc 200
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catcacccag tgtgacatct atagcaccct tctgggcctg cccgctgaca 350
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atcccgagcc aaagacagag tggcggttagc aggtggagtc ttttcatcc 500
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caggttatgt gtgaagaacc aggggccaga gctgggggtt ggctgggtct 850
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<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

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Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
														30

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
														45

Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50	55	60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala		
65	70	75
Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile		
80	85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr		
95	100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala		
110	115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro		
125	130	135
Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro		
140	145	150
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr		
155	160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile		
170	175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr		
185	190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg		
200	205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser		
215	220	225
Leu Thr Gly Tyr Val		
230		

<210> 135

<211> 610

<212> DNA

<213> Homo sapiens

<400> 135

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aagtcatcgc tcccgtggc tcagaaccat ggctgtgcc a cccggcaccc 150
aggtgtggag acaagatcta caaccccttg gagcagtgtct gttacaatga 200
cgccatcgtg tccctgagcg agacccggca atgtggtccc ccctgcaccc 250
tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcacaaac 300
gattttggta tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

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atctccatc tccagtaaat gtgaaaggcag aagacgtttt ccctgagaag 400
acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
aggtaatatg tgtaccagta gagaaggctg aggaatttac aaaatgatgc 500
agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
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acctgtaaaa 610

<210> 136
<211> 119
<212> PRT
<213> Homo sapiens

<400> 136
Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
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Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
20 25 30
Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
35 40 45
Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
50 55 60
Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
65 70 75
Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
80 85 90
Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
95 100 105
Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
110 115

<210> 137
<211> 771
<212> DNA
<213> Homo sapiens

<400> 137
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gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
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gacctgtctg aggcccaccc tgcaagctgcc ctgaggaggc ccacaggtcc 550
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tatgtacttt ataaatgaaa a 771

<210> 138
<211> 110
<212> PRT
<213> Homo sapiens

<400> 138
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Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
20 25 30
Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
35 40 45
Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
50 55 60
Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
65 70 75
Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
. 80 85 90
Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
95 100 105
Cys Arg Ser Val Ser
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<210> 139
<211> 2044
<212> DNA
<213> Homo sapiens

<400> 139

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cccacggccc tggaggccgg cagctggcgc tggggatccc tgctttcgc 200
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tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
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Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
20 25 30

Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
35 40 45

Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
50 55 60

Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
65 70 75

Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
80 85 90

Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
95 100 105

Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
110 115 120

Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
125 130 135

Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140	145	150
Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 gagggtcctc tcctccttgc tggactcgc gctgctctgg ttccccctgg 350
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 agatactccc cggcgagag ctggcaccccc tacttggagc cacaaggcct 450

ESTATE OF

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cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens

<400> 142

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 Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
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 Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
 35 40 45
 Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
 50 55 60
 Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
 65 70 75
 Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
 80 85 90
 Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
 95 100 105
 Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
 110 115 120
 Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro
 125 130 135
 Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys
 140 145 150
 Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro
 155 160 165
 Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu
 170 175 180
 Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg
 185 190 195
 His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly
 200 205 210
 Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe
 215 220 225
 Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val
 230 235 240
 Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly
 245 250 255
 Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg
 260 265 270
 Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly
 275 280 285
 Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
440	445	450

Thr

<210> 143
<211> 693
<212> DNA
<213> Homo sapiens

<400> 143
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cggggagctc ccgtggcgcc tccgctggct gtgcaggcgg ccatggattc 100
cttgcggaaa atgctgatct cagtcgcaat gctggcgca ggggctggcg 150
tgggctacgc gtcctcggtt atcgtgaccc cgggagagcg gcggaaagcag 200
gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
ggcgccagcg ggaggtcacc gtgagaccgg acttgcctcc gtggcgccg 400
gaccttggct tggcgccagg aatccgaggc agcctttctc cttcgtggc 450

ccagcggaga gtccggaccc agataccatg ccaggactct ccggggtcct 500
gtgagctgcc gtcgggtgag cacgttccc ccaaaccctg gactgactgc 550
tttaaggccc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaaaaaaaa 650
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaa 693

<210> 144
<211> 93
<212> PRT
<213> Homo sapiens

<400> 144
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
1 5 10 15
Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
20 25 30
Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
35 40 45
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
50 55 60
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
65 70 75
Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
80 85 90
Arg Ser Pro

<210> 145
<211> 1883
<212> DNA
<213> Homo sapiens

<400> 145
caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgccc 50
ttgaggggaa gaggctgact gtacgttctt tctactctgg caccactctc 100
caggctgcca tggggcccaag caccctctc ctcatcttgt tcctttgtc 150
atggtcggga cccctccaag gacagcagca ccaccttgg gagtacatgg 200
aacgcccact agctgctta gaggaacggc tggcccagtcc 250
agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
acaccatctc cgggagagtg gatcgctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtagc 450
tggaggccct gggaccaaag gcaaggaaag aaggaatgag aagtacgata 500
tgggtacaga ctgtggctac acaatctctc aagttagatc aatgaagatt 550
ctgaagcgat ttgggtggccc agctggctta tggaccaagg atccactggg 600
gcaaacagag aagatctacg tgttagatgg gacacagaat gacacagcct 650
ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccgaaa 700
gcttccccgag tccgggtgcc cttccctgg gttaggcacag ggcagctgg 750
atatggtggc tttctttatt ttgctcgag gcctcctgga agacctggg 800
gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
aaccgaacag tgggtggacag ctcagtattc ccagcagagg ggctgatccc 900
cccctacggc ttgacagcag acacccatcg acacctggta gctgatgagg 950
aaggctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000
ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
accatgtccc agagagaatg ctgaggctgc ctttgcatac tgtggaccc 1100
tctatgtcgt ctataacacc cgtcctgcca gtcgggcccc catccagtgc 1150
tcctttgatg ccagcggcac cctgacccct gaacgggcag cactccctta 1200
ttttccccgc agatatggtg cccatgccag cctccgctat aaccccccag 1250
aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
gagatgagga agaaagagga ggaggttga ggagctagcc ttgtttttg 1350
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ttcctcattc ttcaaattgtg ggccagttgt ggctcaaatc ctctatattt 1450
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ccagatcctg agtaatcctt ttagagcccc aagagtcaaa accctcaatg 1550
ttccctcctg ctctcctgccc ccatgtcaac aaatttcagg ctaaggatgc 1600
cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650
agcagtgttc ttcccctcag agtgacttgg ggagggagaa ataggaggag 1700
acgtccagct ctgtcctctc ttccctcactc ctcccttcag tgtcctgagg 1750
aacaggactt tctccacatt gttttgtatt gcaacattt gcattaaaag 1800
aaaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
1 5 10 15

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
215 220 225

Pro Gly Arg Pro Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
245 250 255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala
260 265 270

Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
275 280 285

Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
290 295 300

Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
305 310 315

Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
320 325 330

Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile
335 340 345

Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
350 355 360

Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
365 370 375

Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
380 385 390

Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu
395 400 405

Val

<210> 147
<211> 2052
<212> DNA
<213> Homo sapiens

<400> 147
gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcct 50
ccgctcacgc agaggctctc cgtggcttcc gcaccttgag cattaggcca 100
gttctcctct tctctcta at ccatccgtca cctctcctgt catccgttcc 150
catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
ttggttctga gtctcctcaa gctggatca gggcagtggc aggtgttgg 250
gccagacaag cctgtccagg ccttgggggg ggaggacgca gcatttcct 300
gtttcctgtc tcctaagacc aatgcagagg ccatgaaagt gcggttctc 350
agggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtaagg 450
attctattgc ggagggggcgc atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
tcgggctgg tccccggcc cacagcgaag tggaaaggc cacaaggaca 700
ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgttg 750
atgtggagat ctctctgacc gtccaagaga acgccggag catatcctgt 800
tccatgcggc atgctcatct gagccgagag gtggaatcca gggtacagat 850
aggagatacc ttttcgagc ctatatcgta gcacctggct accaaagtac 900
tggaaatact ctgctgtggc ctatttttg gcattgttgg actgaagatt 950
ttcttctcca aattccagtg gaaaatccag gcggaaactgg actggagaag 1000
aaagcacgga cagggcagaat tgagagacgc ccggaaacac gcagtggagg 1050
tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg 1100
aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
gagatttaca aggaagagtg tggggcttc tcagagttc caagcaggga 1200
aacattactg ggaggtggac ggaggacaca ataaaaggtg gcgcgtggga 1250
gtgtgccggg atgatgtgga caggaggaag gagtagtga ctggatctcc 1300
cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
cattaaatcc ccgttttac agcgtttcc ccaggacccc acctacaaaa 1400
ataggggtct tcctggacta tgagtgtgg accatctcct tcttcaacat 1450
aaatgaccag tcccttattt ataccctgac atgtcggtt gaaggcttat 1500
tgaggcccta cattgagttt ccgtcctata atgagcaaaa tggaactccc 1550
atagtcatct gcccagtcac ccaggaatca gagaaagagg cctcttggca 1600
aagggcctct gcaatcccag agacaagcaa cagttagtcc tcctcacagg 1650
caaccacgccc ttccctcccc aggggtgaaa tgttaggatga atcacatccc 1700
acattcttct ttagggatataaggatctct ctcccagatc caaagtccc 1750
cagcagccgg ccaaggtggc ttccagatga agggggactg gcctgtccac 1800
atgggagtca ggtgtcatgg ctgcccgtag ctgggaggga agaaggctga 1850
cattacattt agtttgctct cactccatct ggctaagtga tcttgaata 1900
ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttatttgatg 2000
acagagtgtt tcctaatggc ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148
Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly
1 5 10 15

Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala
20 25 30

Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
35 40 45

Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
50 55 60

Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
65 70 75

Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
80 85 90

Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
95 100 105

Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
110 115 120

Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
125 130 135

Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
140 145 150

Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
155 160 165

Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
170 175 180

Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
185 190 195

Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
200 205 210

Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
215 220 225

Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230	235	240
Gly Ile Leu Cys Cys Gly	Leu Phe Phe	Gly Ile Val Gly Leu Lys
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg	Lys
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro	Lys
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Gln Ala	Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgctgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcc a cagtatcaag gcaggacaaa actggtaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcgccg gcggttgcgg aggttcctt 50
ggtcggattt caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc ggcgcatttag gagcctggccg agcctggcg 150
gcctcgccct gttgtgtgc gccggccggc ccggccgcgt cgccctcagcc 200
gcctcgccgg ggaatgtcac cggtgccggc gggggccgcgg ggcaggtgga 250
cgcgatcgccg ggccccgggt tgccggggcga gcccagccac cccttcccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

cacccttctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcgcccc ctcgcccacc acccctccgg cggcgaaacg cacttcgacc 500
acctctcagg cgccgaccag acccgccgacc accacccttt cgacgaccac 550
tggcccgccg ccgaccaccc ctgttagcgac caccgtaccg gcccacga 600
ctccccggac cccgaccccc gatctccca gcagcagcaa cagcagcgtc 650
ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700
tgtatgtaac tgctctgtgg ttgaaagcct gaatgtaat cgctgcaacc 750
agaccacagg gcagtgtgag tgtcgccag gttatcaggg gcttcactgt 800
gaaacctgca aagaggcctt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgttagtccac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga gggtggaact gaagtttatt ttatTTTtagc aaggaaaaaa 950
aaaaggctgc tactctcaag gaccatactg gttaaacaa aggaggatga 1000
gggtcataga tttacaaaat attttatata cttttattct cttaacttat 1050
atgttatatt taatgtcagg attaaaaaac atctaattta ctgatTTAGT 1100
tcttcaaaag cactagagtc gccaattttt ctctggata atttctgtaa 1150
atttcatggg aaaaaattat tgaagaataa atctgcttgc tggaaggcgt 1200
ttcaggcatg aaacctgcta ggaggTTAG aaatgttctt atgtttatta 1250
atataccatt ggagTTGAG gaaatttGTT gttggTTA ttttctctc 1300
taatcaaaaat tctacatTTG tttcttggaa catctaaAGC ttaacctggg 1350
ggtaccctaa tttatTTAAC tagtggtaa tagactggTT ttactctatt 1400
taccagtaca ttttggagac caaaagtaga ttaagcagga attatcttta 1450
aactattatg ttatTTGGAG gtaatttaat ctgtggaaat aatgtactgt 1500
tatctaagca tttgcTTGT actgcactga aagtaattat tcttgacct 1550
tatgtgaggc acttggctt ttgtggaccc caagtcaaaa aactgaagag 1600
acagtattaa ataatgaaaa aaataatgac aggttatact cagtgtacc 1650
tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttggca 1700
agtaatttcc tttcactgag cttgtttctt ctcaaggTTG ttgtgaagat 1750
taaatgagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800
ctggTTTGTt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgtttaaga acttttagct ccttgacaaa gaagtgcctt atactttagc 1900
actaaatatt ttaaatgctt tataaatgat attatactgt tatggaatat 1950
tgtatcatat tgtatgttat taaaaatgta gaagaggctg ggccgcgtgg 2000
ctcacgcctg taatcctagc actttgggag gccaaaggcg gtggatcact 2050
tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgct 2100
ctactaaaaa tacaaacaaa ttagctggc gtggtggcac acacctgtag 2150
tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
tggaggttgc agtgagctga gatcgccca ctgcactcca gcctggtag 2250
agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
1 5 10 15

Ala Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn
20 25 30

Val Thr Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
35 40 45

Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
50 55 60

Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
65 70 75

Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
80 85 90

Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
95 100 105

Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
110 115 120

Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
125 130 135

Thr Thr Leu Ser Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
140 145 150

Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
155 160 165

Asp Leu Pro Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

170 175 180

Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn
185 190 195

Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr
200 205 210

Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys
215 220 225

Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu
230 235 240

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
245 250 255

Cys Asn Arg

<210> 154
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 154
aactgctctg tggttgaaag cctg 24

<210> 155
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 155
cagtacatg gctgacagac ccac 24

<210> 156
<211> 38
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-38
<223> Synthetic construct.

<400> 156
aggatatcg gggcttcaact gtgaaaacctg caaagagg 38

<210> 157
<211> 689
<212> DNA
<213> Homo sapiens

<400> 157
tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
ttctggctt ggtctcggtg cccagggccc aggccgtgtg gttggaaaga 100
ctggaccctg agcagcttct tggccctgg tacgtgcttg cggtggcctc 150
ccggaaaaag ggcttgcca tggagaagga catgaagaac gtctgtgggg 200
tggtgtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
cacgggctgg gagggtgtga ccagagtgtc atggacctga taaagcgaaa 300
ctccggatgg gtgttgaga atccctcaat aggcgtgctg gagctctggg 350
tgctggccac caacttcaga gactatgccca tcatttcac tcagctggag 400
ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
agccagccag gaggccatgg ggctttcac caagtggagc aggagcctgg 500
gcttcctgtc acagtagcag gcccagctgc agaaggacct cacctgtgct 550
cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600
gggtcctgtg acctcggcca gtgtccaccc acctcgctca gcggctcccg 650
gggcccagca ccagtcaga ataaagcgat tccacagca 689

<210> 158
<211> 163
<212> PRT
<213> Homo sapiens

<400> 158
Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
1 5 10 15
Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
20 25 30
Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
35 40 45
Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
50 55 60
Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
65 70 75
His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
95 100 105

Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
110 115 120

Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
125 130 135

Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
140 145 150

Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
155 160

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

aacagacgtt ccctcgccgc cctggcacct ctaaccaggc acatgctgct 50
gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100
gtaaaactgct gacgatgcag agttccgtga cggtgcagga aggctgtgt 150
gtccatgtgc cctgctcatt ctcctacccc tcgcattggct ggatttaccc 200
tggcccagta gttcatggct actgggtccg ggaaggggcc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctcggcagt gtgggaggag 300
actcgggacc gattccaccc ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgccca gaagaagtga tgcggggaga tacttcttc 400
gtatggagaa aggaagtata aaatggatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccccc agaatctgac ctgctctgtc ccctgggcct 550
gtgagcaggg gacacccct atgatctcct ggataggac ctccgtgtcc 600
ccccctggacc cctccacccac ccgctcctcg gtgctcaccc tcataccaca 650
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
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cttgggaaat ggctcatctc tgtcaactccc agagggccag tctctgccc 850
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
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ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050
ctgcagagca aagccacatc aggagtact cagggggtgg tcgggggagc 1100
tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgtttag 1150
tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtggagat 1200
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atgaattatg tgcagagtga aaagcacaca ggcttagag tcaaagtatc 1600
tcaaacctga atccacactg tgccctccct tttttttt taactaaaag 1650
acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1														15

Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
														30

Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
														45

Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
														60

Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
														75

Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
														90

Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
														105

Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

110	115	120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu		
125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile		
140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser		
155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp		
170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser		
185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser		
200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn		
215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr		
230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly		
245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu		
260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu		
275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser		
290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala		
305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln		
320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val		
335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe		
350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Arg Ser Cys Arg Lys		
365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu		
380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
410 415 420

Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
425 430 435

Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
440 445 450

Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
455 460

<210> 161
<211> 739
<212> DNA
<213> Homo sapiens

<400> 161
gacggccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
tcgataagga ctittccggag gacaggaggc ccaggaaggt gtccccagtg 200
aaggtgacag ccctgggcgg tggaaagttg gaagccacgt tcaccttcat 250
gagggaggat cggtgcattcc agaagaaaaat cctgatgcgg aagacggagg 300
agcctggcaa atacagcgcc tatggggca ggaagctcat gtacctgcag 350
gagctgcccga ggagggacca ctacatctt tactgcaaag accagcacca 400
tgggggcctg ctccacatgg gaaagcttgt ggtaggaat tctgatacca 450
accgggaggc ccttggaaat tttaagaaat tggtgacgcg caagggactc 500
tcggaggagg acatttcac gcccctgcag acgggaagct gcgttcccga 550
acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
acacagagcc cggaccacct ggacctaccc tccagccatg acccttcct 650
gctcccaccc acctgactcc aaataaaagtc ctttcccccc aaaaaaaaaa 700
aaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
<211> 170
<212> PRT
<213> Homo sapiens

<400> 162
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
1 5 10 15

Leu Ser Phe Thr Leu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20	25	30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg		
35	40	45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly		
50	55	60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile		
65	70	75
Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr		
80	85	90
Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro		
95	100	105
Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly		
110	115	120
Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr		
125	130	135
Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys		
140	145	150
Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser		
155	160	165
Cys Val Pro Glu His		
170		
<210> 163		
<211> 22		
<212> DNA		
<213> Artificial		
<220>		
<221> Artificial Sequence		
<222> 1-22		
<223> Synthetic construct.		
<400> 163		
ggagatgaag accctgttcc tg 22		
<210> 164		
<211> 26		
<212> DNA		
<213> Artificial		
<220>		
<221> Artificial Sequence		
<222> 1-26		
<223> Synthetic construct.		
<400> 164		
ggagatgaag accctgttcc tgggtg 26		

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<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cgggAACGCA gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
caggacactg gtacgtgaag gccatggtgg tcgataagga cttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccTTca ccctggagga ggaggatATC acAGGGACCT ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagagggtt gaggtggctg cgggactgga agtcatcggg 50
cagaggcttc acagcagcca aggaacctgg ggcccgctcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150
gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtgggg 250
cgacgctcat cgcccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgctaca tagttcacct gggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccggacag ccactgagtc cttcccccac cccggcttca 400
acaacagcct ccccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctggct gtgcgacccc tcaccctctc 500
ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
gcacgtccag cccccagttt cgcctgcctc acaccttgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgttag aacgcctacc ccggcaacat 650
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccagggtga ctccgggggc cctctggct gtaaccagtc tcttcaaggc 750
attatctcct ggggccagga tccgtgtcg atcacccgaa agcctggtgt 800
ctacacgaaa gtctgcaaataat atgtggactg gatccaggag acgatgaaga 850
acaatttagac tggacccacc caccacagcc catcaccctc catttccact 900
tggtgtttgg ttccctgttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050
ccttgaataa ttgtgactct ggaaatgaca acacctggtt tggtctctgt 1100
tgtatccccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15

Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
 20 25 30
 His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
 35 40 45
 Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
 50 55 60
 Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
 65 70 75
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
 80 85 90
 Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
 95 100 105
 Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val
 110 115 120
 Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
 125 130 135
 Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr
 140 145 150
 Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn
 155 160 165
 Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly
 170 175 180
 Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly
 185 190 195
 Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
 200 205 210
 Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
 215 220 225
 Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
 230 235 240
 Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
 245 250

<210> 171
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 171
ggctgcggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtatgt tgccgggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgttagaca ccaggtttc gggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176
cccttgatga tcctggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178
gagagaccag gatcatcaag gggttcgagt gcaaggctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179
gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50
gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100
aagaaaagagg agagcaccga agaagtgaaa atagaagttt tgcatcgccc 150
agaaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200
atgacggcta cctggctaaa gacggctcgaa aattctactg cagccggaca 250
caaaaatgaag gccaccccaa atggttgtt cttgggtttg ggcaagtcat 300
aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattt aactttatgc 450
tgtgacccaa ggaccacgga gcattgagac atttaaacaat atagacatgg 500
acaatgacag gcagctctaa agccgaga taaacctcta cttgcaaagg 550
gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
tttagaagat attttaaga agaatgacca tgatggatggatggcttcattt 650
ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
atttctactt tttttttta gctatttact gtactttatg tataaaacaa 750
agtcactttt ctccaagttt tatttgctat ttttccccta tgagaagata 800
ttttgatctc cccaatacat tgattttggat ataataaaatg tgaggctgtt 850
ttgcaaactt aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaa 900
aaaaaaaa 907

<210> 180

<211> 222

<212> PRT

<213> Homo sapiens

<400> 180

Met	Pro	Lys	Thr	Met	His	Phe	Leu	Phe	Arg	Phe	Ile	Val	Phe	Phe
1				5				10					15	

Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu
				20				25					30	

Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn
				35				40				45		

Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr
				50				55				60		

Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg
				65				70				75		

Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly
				80				85				90		

Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro
				95				100				105		

Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly
				110				115				120		

Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu
				125				130				135		

Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser
				140				145				150		

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu
155 160 165

Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu
215 220

<210> 181
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-22
<223> Synthetic construct.

<400> 181
gtgttctgct ggagccgatg cc 22

<210> 182
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 182
gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 183
cctttcagga tgtaggag 18

<210> 184
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcacccatgtat atgacttgat acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagagg aagaggagg 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
gcccatatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
cagaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaacccaaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150
atacttctgg atctggcag aaactattca cattcccctt ggagacatgt 200
aacgccaggc atggcggctc gcgcctgtaa tcccagtct ttggaaagcc 250
aaggcaggta gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cggcggttgt 350
ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
cttgaactca ggaggcagaa gttcagtga acccagatcc tgccattgca 450
ctccagcatg gatgacagag caagactccg tctaaaaag aaaagatagt 500
ttcttgcgttc atttcgcac tgccctctca gtgttcctg ggatccccctc 550
ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5					10				15	
Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20				25					30	
Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35				40					45	
Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50				55					60	
Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu	
				65				70						

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgcggccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtgaaaaac acagggaaag ggtgacctct gagattcccc tttccccc 100
gactttggaa gtgacccacc atggggctca gcatctttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacacccg aagatttca atggcactga 200
gtgtggcgt aactcacagc cgtggcaggt gggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcaactgca gcggcagcag gtactgggtg cgcctgggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatccccg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
ctgctgcggc tgcgcctgcc cgtcccgta accagcagcg ttcaacccct 500
gccccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
gctggggcat caccaaccac ccacggAACc cattcccgga tctgctccag 600
tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
cgggagaatc acgagcaaca tggtgtgtgc aggccggcgtc ccggggcagg 700
atgcctgcca gggtgattct gggggccccc tggtgtgtgg gggagtcctt 750
caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

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ccctagctcc actcttgttg gcctggaaac ttcttggaaac tttaactcct 1000
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<210> 194
<211> 248
<212> PRT
<213> Homo sapiens

<400> 194
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1 5 10 15
Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
20 25 30
Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
35 40 45
Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
50 55 60
Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
65 70 75
Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
80 85 90
Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
95 100 105
Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
110 115 120
Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
125 130 135
Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
140 145 150
Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
155 160 165
Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
170 175 180
Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
185 190 195
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

200 205 210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp
215 220 225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp
230 235 240
Ile Arg Met Ile Met Arg Asn Asn
245

<210> 195
<211> 1485
<212> DNA
<213> Homo sapiens

<400> 195
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tcgcacatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
ggcttgctca aagcccgga aagaggagg ctggccgaga tcaaccggga 200
gtttctgtgt gaccagaagt acagtgtatga agagaacctt ccagaaaagc 250
tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
gagattgacc tgatgtctt aaagaggatg atggagaagc ttgggtgtccc 350
caagacccac ctggagatga agaagatgat ctcagaggtg acaggagggg 400
tcagtgacac tatatacctac cgagactttg tgaacatgat gctggggaaa 450
cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
gagcagcccc aagccagttg gccccctcc agagagagac attgcttagcc 550
tgccctgagg accccgcctg gactccccag cttcccccacc ccataccctcc 600
ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
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ttgggtcccc tccctctttt cttccctcct tccccgcctc ctgtgcagaa 800
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tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950
gaccccaaggc cactctgaga agaccttgga gtagggacaa ggctgcaggg 1000
cctctttcgg gtttccttgg acagtgccat ggttccagtg ctctgggtgc 1050

acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100
attccacacc tcttctcatc ctcagtatg tgaagggtggg aaggaaagga 1150
gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200
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gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
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tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe	
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Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn	
			20				25					30			
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu	
				35				40					45		
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp	
				50				55				60			
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met	
				65				70				75			
Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys	
				80				85				90			
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr	
				95				100				105			
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu	
				110				115				120			
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro	
				125				130				135			
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro	
				140				145				150			

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
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cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataat 300
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg
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Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ser	Val	Leu	Ser	Gly	Pro	Pro	
				20				25				30		
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val
			35				40				45			
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro
			50				55			60				
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg
			65				70				75			
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu
			80				85			90				
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe
			95				100			105				
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys
			110				115			120				
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu
			125				130			135				
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg
			140				145			150				
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp
			155				160			165				

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu
 170 175 180
 Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Ile Ser Arg
 185 190 195
 Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu
 200 205 210
 Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp
 215 220 225
 Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr
 230 235 240
 Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp
 245 250 255
 Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro
 260 265 270
 Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr
 275 280 285
 Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu
 290 295 300
 Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu
 305 310 315
 Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr
 320 325 330
 Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp
 335 340 345
 Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu
 350 355 360
 Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe
 365 370 375
 Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Asn Ala Asn Lys
 380 385 390
 Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu
 395 400 405
 Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys
 410 415 420
 Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala
 425 430 435
 Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp
 440 445 450
 Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser

455	460	465
Ser Pro Arg Arg	Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser
470	475	480
Lys Lys Phe Arg Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe		
485	490	495
Ser Ser Glu Cys Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg		
500	505	510
Cys Glu Gly Thr Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg		
515	520	525
Ile Pro Ser His Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn		
530	535	540
Asp Asn Glu Val Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys		
545	550	555
Leu Pro Asn Leu Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys		
560	565	570
Glu Val Arg Glu Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu		
575	580	585
Leu Met Leu Thr Gly Asn Gln Leu Glu Thr Val His Gly Arg Val		
590	595	600
Phe Arg Gly Leu Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn		
605	610	615
Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser		
620	625	630
Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr		
635	640	645
Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu		
650	655	660
Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly		
665	670	675
Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys		
680	685	690
Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala		
695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln		
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val		
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met		
740	745	750

Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr
 755 760 765
 Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile
 770 775 780
 Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe
 785 790 795
 Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg
 800 805 810
 Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu
 815 820 825
 Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu
 830 835 840
 Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly
 845 850 855
 Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu
 860 865 870
 Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser
 875 880 885
 Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr
 890 895 900
 His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala
 905 910 915
 Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr
 920 925 930
 Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr
 935 940 945
 Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile
 950 955 960
 Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser
 965 970 975
 His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly
 980 985 990
 Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys
 995 1000 1005
 Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys
 1010 1015 1020
 Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile
 1025 1030 1035
 Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys

1040 1045 1050

Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly
1055 1060 1065

Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala
1070 1075 1080

His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly
1085 1090 1095

Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu
1100 1105 1110

His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln
1115 1120 1125

Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu
1130 1135 1140

Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu
1145 1150 1155

Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu
1160 1165 1170

Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln
1175 1180 1185

Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp
1190 1195 1200

Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu
1205 1210 1215

Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val
1220 1225 1230

Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr
1235 1240 1245

Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys
1250 1255 1260

Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser
1265 1270 1275

Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala
1280 1285 1290

Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys
1295 1300 1305

Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala
1310 1315 1320

Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys
1325 1330 1335

PROTEIN SEQUENCE

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser
1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctccctg agctgcctgt caccgactag gtggagcagt 50
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gcccccacgg tcctggatga cggcagcatc 350
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgccca ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaaag gctgtgaggt ttcctaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtgaa tgtccaaatg 650
cctgtgtcat cttgtcccgt ttcctcccaa tattccttct caaacttgga 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaaat 750
gtc 753

<210> 203
<211> 148
<212> PRT
<213> Homo sapiens

<400> 203
Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
1 5 10 15

Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
20 25 30

Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
35 40 45

Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
50 55 60

Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
65 70 75

Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
80 85 90

Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
95 100 105

Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
110 115 120

Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
125 130 135

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
140 145

<210> 204
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 204
gcaggcttg aggatgaagg ctgc 24

<210> 205
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctgcaggcgt ggctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
cagggcattt gcatcccact gtccttgtt tcggagccag gccacaccgt 50
cctcagcagt gtcatgtgtt aaaaacgccca agctgaatat atcatgcccc 100
tataaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaaagaag atcctattt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350
cacagctgct gttttaagg aaacattcaa gtccctgtct cacatagacc 400
ctgatgtcct ctatccatct ctaaatgtca ccagcttga ctcaagtgtt 450
cctgaaaagc tggatgacct agtccccaa gggaaaaaat tcctgctgct 500
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tgtcattcca tgttcagcag agtattttaa ttatatttc tcgggattat 1350
tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggtttc 1400
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ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500
tcactgtcat ctgttaggga atttttgttt gtcctgtctt tgcctggatc 1550
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actgagatataaaaaggt gtttatcata aaaaaaaaaa aaaaaaaaa 1648

<210> 210
<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly
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Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val
20 25 30

Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
35 40 45

Phe Pro Asp Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
50 55 60

Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
65 70 75

Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
80 85 90

Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
95 100 105

Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
110 115 120

Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
125 130 135

Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
140 145 150

Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp
155 160 165

Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg
170 175 180

Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val
185 190 195

Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe
200 205 210

Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val
215 220 225

Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
230 235 240

Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly
245 250 255

Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu
260 265 270

```
<210> 211  
<211> 1554  
<212> DNA  
<213> Homo sapiens
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<400> 211
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tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaa 200
tttgcatgag ttccctgggtta atttgcatga gagatatggg cctgtggct 250
ccttctgggtt tggcaggcgc ctgcgtgggtta gtttgggcac tggtgatgta 300
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
gctgaagtca ttatataaggat atcaatctgg tgggtggcagt gtgagtgaaa 400
accacatgag gaaaaaaattt tatgaaaatg gtgtgactga ttctctgaag 450
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gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttgc 550
gttttgcata gaagtctgtt acacagatgg taatgggttag tacatttgc 600
gatgatcagg aagtcatcg cttccagaag aatcatggca cagtttggc 650
tgagatggaa aaggcttcc tagatggc acttgataaa aacatgactc 700
ggaaaaaaaca atatgaagat gccctcatgc aactggagtc tgtttaagg 750
aacatcataa aagaacgaaa aggaaggaac ttcatcgaaac atatttcat 800
tgactcctta gtacaaggaa accttaatga ccaacagatc ctggaaagaca 850
gtatgatatt ttctctggcc agttgcataa taactgc当地 attgtgtacc 900
tggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccqagqaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
gccaaactga ctccagttc tgcccagctt caagatattg aaggaaaaat 1100
tgaccgattt attattccta gagagaccct cgtccttat gcccttggtg 1150
tggtacttca ggatccta atctggccat ctccacacaa gtttgatcca 1200
gatcggtttg atgatgaatt agtaatgaaa acttttcct cacttggatt 1250
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ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaga 1400
agcttggatc actgtctcaa agagatatta aaattttata catttaaat 1450
cattgttaaa ttgattgagg aaaacaacca tttaaaaaaaaa atctatgtt 1500
aatcctttta taaaccagta tcactttgtatataaaacac ctatggat 1550
ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
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Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala
					20				25					30

Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu
								35	40					45

Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn
									50	55				60

Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg
									65	70				75

Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His
									80	85				90

Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys
									95	100				105

Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Ser	Val	Ser	Glu	Asn	
									110	115				120

His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu
									125	130				135

Lys Ser Asn Phe Ala Leu Leu Lys Leu Ser Glu Glu Leu Leu

	140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser			
155	160	165	
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val			
170	175	180	
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln			
185	190	195	
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu			
200	205	210	
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu			
215	220	225	
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys			
230	235	240	
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser			
245	250	255	
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser			
260	265	270	
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys			
275	280	285	
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys			
290	295	300	
Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val			
305	310	315	
Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu			
320	325	330	
Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln			
335	340	345	
Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg			
350	355	360	
Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro			
365	370	375	
Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp			
380	385	390	
Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly			
395	400	405	
Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr			
410	415	420	
Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val			
425	430	435	

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213
<211> 759
<212> DNA
<213> Homo sapiens

<400> 213
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tcagggcttg tgccctctcg ctccctgacg ctccctggcgc atctggtggt 150
cgtcatcacc ttattctggc cccggggacag caacatacag gcctgcctgc 200
ctctcacgtt cacccccgag gagtatgaca agcaggacat tcagctggtg 250
gccgcgcgtct ctgtcacccct gggcctcttt gcagtggagc tggccgggtt 300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
gggctcactg tagtgcattcc gtggccctgt ctttcttcat attcgagcgt 400
tgggagtgca ctacgtattt gtacattttt gtcttctgca gtgcccttcc 450
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ggcaaggggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggtt 600
ttcccctcgg aaactgcattc tgctggagga tatgtgttgg aataattacg 650
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaaata 700
tgtttgttag taacattaag acttatatac agtttttaggg gacaattaaa 750
aaaaaaaaa 759

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
1 5 10 15
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

<210> 215

<211> 697

<212> DNA

<213> Homo sapiens

<400> 215

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gaccggcct gctgcagccc catagtgccc cggaacgagt ggaaggccct 150
ggcatcagag tgcgcccagc acctgaggct gcccttacgc tatgtggtgg 200
tatcgacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgca 300
cgtggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gcccactcag gtcacttatg gaacccatg 400
tccattggca tcagttcat gggcaactac atggatcggg tgcccacacc 450
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acactctctc caggcaacca gcttaccac ctcatccaga attggccaca 600
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctccctcc 650
catggccaaa aaccccactg tctcattctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu
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Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys
					20				25					30
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu
					35				40					45
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser
					50				55					60
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln
					65				70					75
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp
					80				85					90
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Ile	Gly	Glu	Asp	Gly	Leu	Val	
					95				100					105
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His
					110				115					120
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
					125				130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
					140				145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
					155				160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
					170				175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
					185				190					195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggc catctgtggc caggatgatg gtccctccgg ctcagaggac 150
cctgagcgtg atgaccacgaa gggccagccc cggccccggg tgccctcgaa 200

gcggggccac atctcaccta agtcccggcc catggccaat tccactctcc 250
tagggctgct ggccccgcct ggggaggcct ggggcattct tgggcagccc 300
cccaaccgccc cgaaccacag ccccccaccc tcagccaagg tgaagaaaaat 350
cttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
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aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
gaacggggcc gccggaccc tcgttgcacc cacgaccagg ccaagatctg 650
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aaccgctgat tgctgacttt tgtgtgaaga atcgtttct tggagcagga 1850
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<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

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Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
				20				25				30		
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
				35				40				45		
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met
				50				55				60		
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala
				65				70				75		
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro
				80				85				90		
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe
				95				100				105		
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly
				110				115				120		
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln
				125				130				135		
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro
				140				145				150		
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile
				155				160				165		
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu
				170				175				180		
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro
				185				190				195		
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp
				200				205				210		

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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gggttctgca ttagtcctt aaaggacaaa ggtaacagag ccagcgagag 150
agctcgaggg gagactttga cttaagcca cagaatttgtt ggaagtgtgc 200
gcgccgcccgc cgccgtcgct cctgcagcgc tgtcgaccta gccgctagca 250
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agcgccagcc ggctgcggct gcccacacgg ctcaccatgg gctccggcg 350
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ggctgcccgt ctgggcacag aacgacacgg agcccatcggt gctggaggcg 450
aagtgtctgg tgggtgtgcga ctgcAACCCG gccacggact ccaagggtctc 500
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tttcacattt gagtctgtct ttgttagcacc aagaaaagga atttacagtt 700
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ttcaaatatc ccataatctaa atttagtgca atatcttgc ttttgtatag 2000
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tatatgttaa aaaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu
1 5 10 15

Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
20 25 30

Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
35 40 45

Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Pro Leu
50 55 60

Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala
65 70 75

Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
80 85 90

Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
95 100 105

Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
110 115 120

Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
125 130 135

Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
140 145 150

Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
155 160 165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
185 190 195

Phe Leu Val Phe Pro Leu
200

<210> 221

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 221

acggctcacc atgggctccg 20

<210> 222

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 222

aggaagagga gcccttggag tccg 24

<210> 223

<211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cgtgctggag ggcaagtgtc tgggggtgtc cgactcgaaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
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tttcgtccct tgtttgggtc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcggttg tctctgtcta 250
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gtgaagggtt gaagagtata aacccaggtg agacagcacc ctctatgcga 350
ctgctggcct atgtttctgg cttggcctt ggaatcatga gtggagtatt 400
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ttcatggaga ttctcctcaa ttcttccttt attcagctt catgacgctg 500
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tcagcattta taatccttgt gctcatggc acctggcat tcttagctgc 700
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ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
1 5 10 15

Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu
20 25 30

Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
35 40 45

Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
50 55 60

Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
65 70 75

Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
80 85 90

Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
95 100 105

Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
110 115 120

Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
125 130 135

Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
140 145 150

Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
155 160 165

Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
170 175 180

Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
185 190 195

His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
200 205 210

Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
215 220 225

Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
230 235 240

Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
245 250 255

Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226
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gagccatctg ggggttctgg ggcccaagaa cgtctcgacaa aaagacgccc 150
agtttgagcg cacctacgtg gacgaggta acagcgagct ggtcaacatc 200
tacacccatca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250
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tcagcccccc accaagaatg agtcggagat tcagttttc tacgtggatg 450
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20				25				30		

Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser
 35 40 45
 Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
 50 55 60
 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
 65 70 75
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
 80 85 90
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
 95 100 105
 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
 110 115 120
 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser
 125 130 135
 Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg
 140 145 150
 Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn
 155 160 165
 Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu
 170 175 180
 Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe
 185 190 195
 Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr
 200 205 210
 Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met
 215 220 225
 Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
 230 235 240
 Asn Ser Phe Tyr Val Val Val Val Lys Thr Glu Asp Gln Ala
 245 250 255
 Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro
 260 265 270
 Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser
 275 280 285
 Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys
 290 295 300
 Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala
 305 310 315
 Cys Trp Glu Asn Trp Arg Gln Lys Lys Thr Leu Leu Val Ala

	320	325	330
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala			
335	340	345	
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly			
350	355	360	
Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser			
365	370	375	
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe			
380	385	390	
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val			
395	400	405	
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys			
410	415	420	
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala			
425	430	435	
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe			
440	445	450	
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val			
455	460	465	
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn			
470	475	480	
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly			
485	490	495	
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile			
500	505	510	
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile			
515	520	525	
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu			
530	535	540	
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr			
545	550	555	
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys			
560	565	570	
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met			
575	580	585	
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro			
590	595	600	
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile			
605	610	615	

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn
					620			625				630		
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr
				635				640			645			
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu
				650				655			660			
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp
				665				670			675			
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val
				680				685			690			
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr
				695				700			705			
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala
				710				715			720			
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile
				725				730			735			
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu
				740				745			750			
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe
				755				760			765			
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser
				770				775			780			
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp
				785				790			795			
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser
				800				805			810			
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln
				815				820			825			
Arg	Asp	Lys	Ile	Tyr	Val	Phe								
				830										

<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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ttggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150

gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc 200

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accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgta 300
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
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Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

20	25	30
Glu Asn Tyr Gly Gly Asn Phe Pro Leu Tyr	Leu Thr Lys Leu Pro	
35	40	45
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val	Leu Ser Gly Asp	
50	55	60
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met	Asp Pro Asp Ser	
65	70	75
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg	Glu Glu Gln Ala	
80	85	90
Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln	Asp Gly His Val	
95	100	105
Leu Trp Gly Pro Gln Pro Val Leu Val His Val	Lys Asp Glu Asn	
110	115	120
Asp Gln Val Pro His Phe Ser Gln Ala Ile	Tyr Arg Ala Arg Leu	
125	130	135
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu	Phe Leu Glu Ala	
140	145	150
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser	Asp Leu Arg Phe	
155	160	165
His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser	Pro Asp Met Phe	
170	175	180
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu	Ser Pro Lys Gly	
185	190	195
Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr	Tyr Gln Leu Leu	
200	205	210
Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser	Gly His Gln Ala	
215	220	225
Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser	Thr Trp Val Ser	
230	235	240
Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys	Val Leu Tyr Pro	
245	250	255
His His Met Ala Gln Val His Trp Ser Gly Gly	Asp Val His Tyr	
260	265	270
His Leu Glu Ser His Pro Pro Gly Pro Phe Glu	Val Asn Ala Glu	
275	280	285
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg	Glu Ala Gln Ala	
290	295	300
Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser	His Gly Glu Asp	
305	310	315

Tyr Ala Ala Pro Leu Glu Leu His Val Leu Val Met Asp Glu Asn
 320 325 330
 Asp Asn Val Pro Ile Cys Pro Pro Arg Asp Pro Thr Val Ser Ile
 335 340 345
 Pro Glu Leu Ser Pro Pro Gly Thr Glu Val Thr Arg Leu Ser Ala
 350 355 360
 Glu Asp Ala Asp Ala Pro Gly Ser Pro Asn Ser His Val Val Tyr
 365 370 375
 Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala
 380 385 390
 Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu
 395 400 405
 Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met
 410 415 420
 Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val
 425 430 435
 Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile
 440 445 450
 Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro
 455 460 465
 Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu
 470 475 480
 Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr
 485 490 495
 Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val
 500 505 510
 Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser
 515 520 525
 His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly
 530 535 540
 Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val
 545 550 555
 Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu
 560 565 570
 Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr
 575 580 585
 Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu
 590 595 600
 Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly

605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly Asp	
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr Leu	
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp His	
650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala Ser	
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val	
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr	
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu	Pro Arg Glu His Ile Ile	
710	715	720
Pro Val Val Val Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val	
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg	
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val	
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile	
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser	Arg Lys Lys Asp Pro Asp	
785	790	795
Gln Pro Ala Asp Ser Val Pro Leu Lys	Ala Thr Val	
800	805	

<210> 230

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 230

cgccttaccg cgcaagccga agattcacta tggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Seqeunce

<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aaccccactc cagg 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagtctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
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cagaaatgga gacgagatca gcaaatttagt tcaactatgt aattcaaaca 150
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
gatgtcctgg tccccatctgt cagtcgtcag gcatttaaat ctttcctgag 250
atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaaggcga agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaaag ctatccatca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450
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<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
170 175 180

His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
185 190 195

Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser
200 205 210

Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro
215 220 225

Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
230 235 240

Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro
245 250 255

Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp
260 265 270

Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu
275 280 285

Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn
290 295 300

Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met
305 310 315

Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu
320 325 330

Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val
335 340 345

Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr
350 355 360

Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile
365 370 375

Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly
380 385 390

Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr
395 400 405

Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu
410 415 420

Tyr

<210> 235
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 235

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<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys
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Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr
				20				25					30	
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr
				35				40					45	
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val
				50				55					60	
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val
				65				70					75	
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr
				80				85					90	
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr
				95				100					105	
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser
				110				115					120	
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala
				125				130					135	
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly
				140				145					150	
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe
				155				160					165	
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys
				170				175					180	
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp
				185				190					195	
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala

200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe		
215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met		
230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn		
245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe		
260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala		
275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys		
290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser		
305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala		
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser		
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser		
350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile		
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn		
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile		
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser		
410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

L
I
B
R
A
R
Y
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R

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
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<222> 1-24
<223> Synthetic construct.

<400> 240
ggatataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactcttc tggtggcctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
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ctttctcaag aatcctctgt tctttgcctt ctaaagtctt ggtacatcta 200
ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250
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gcactgcccac caactctgag tccagcacaa cctccagtgg ggtcagcaca 1450
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A
B
D
D
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<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
1				5				10					15	

Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20				25				30		

Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35				40				45		

Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50				55				60		

Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65				70				75		

Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala
 80 85 90
 Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala
 95 100 105
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 110 115 120
 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val
 125 130 135
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala
 140 145 150
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 155 160 165
 Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala
 170 175 180
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 185 190 195
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 200 205 210
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 215 220 225
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 230 235 240
 Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala
 245 250 255
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 260 265 270
 Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
 275 280 285
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 290 295 300
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 305 310 315
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala
 320 325 330
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
 335 340 345
 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala
 350 355 360
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala

365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala		
380	385	390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala		
395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala		
410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala		
425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val		
440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala		
455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala		
470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala		
485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile		
500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe		
515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn		
530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly		
545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro		
560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile		
575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro		
590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26
<210> 245
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic sequence.

<400> 245
gtcagagttg gtggctgtgc tagc 24

<210> 246
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 246
ggaccaggc atttgcctt ccagccacaa agagacagat gaagatgc 48

<210> 247
<211> 957
<212> DNA
<213> Homo sapiens

<400> 247
gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcattcc 50
ttcccgacct tcccagcaat atgcatttg cacgtctggt cggtccctgc 100
tccctccttc tgctactggg ggcctgtct ggatggcg 150
ccccatttgag aaggtcattt aaggatcaa ccgagggtg agcaatgcag 200
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcatt 250
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ctggaaagg 550
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gaagcttggc caaggtgccc accatgctgc

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<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu
1					5				10					15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu
				20					25					30
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg
				35					40					45
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His
				50				55						60
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met
				65				70						75
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu
				80				85						90
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile
				95				100						105
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn
				110				115						120
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln
				125				130						135
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys
				140				145						150
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu
				155				160						165
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala
				170				175						180

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195
Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210
Ser Ser His Gln Gly Gly Ala Thr Thr Pro Leu Ala Ser Gly
215 220 225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240
Ser Val Ala Asn Ile Met Pro
245

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttccttcc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgaccattt gagaaggta ttgaaggat caaccgaggg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252
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tgaccctgac tcactccagg tccggaggcg gggggcccccg gggcgactcg 150
ggggcggacc gcggggcgga gctgccgccc gtgagtcgg ccgagccacc 200
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TRANSLATION

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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro
1					5				10					15

Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Lew	Leu	Leu	Leu	Leu	Leu
				20					25					30

Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
					35				40					45

Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60

Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
					65				70					75

Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80	85	90
Phe Ala Leu Ser Ser Asn Leu Ser Phe		
95	100	105
Gly	Gly	Glu
Leu	Leu	Leu
Trp	Gly	Ala
110	115	120
Asp	Asp	Lys
Ala	Glu	Lys
	Gln	Gln
	Cys	
Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile		
125	130	135
Lys Ile Leu Leu Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly		
140	145	150
Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr Ile Asn Met Glu Asn		
155	160	165
Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val Leu Leu Glu Asp		
170	175	180
Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala		
185	190	195
Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe		
200	205	210
Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg Pro		
215	220	225
Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe		
230	235	240
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly		
245	250	255
Asp Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu		
260	265	270
Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile		
275	280	285
Cys Lys Gly Asp Glu Gly Glu Arg Val Leu Gln Gln Arg Trp		
290	295	300
Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp		
305	310	315
Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro		
320	325	330
Ser Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr		
335	340	345
Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val		
350	355	360
Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys		
365	370	375

Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro
380 385 390

Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg
395 400 405

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu
410 415 420

Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser
425 430 435

Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala
440 445 450

Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe
455 460 465

Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
470 475 480

Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly
485 490 495

Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu
500 505 510

Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn
515 520 525

Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp
530 535 540

Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu
545 550 555

Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu
560 565 570

Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser
575 580 585

Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln
590 595 600

Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser
605 610 615

Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn
620 625 630

Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu
635 640 645

Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu
650 655 660

Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val

665 670 675

Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro
680 685 690

Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys
695 700 705

Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val
710 715 720

Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe
725 730 735

Leu Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln
740 745 750

Gly Glu Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu
755 760 765

Pro Pro Glu Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr
770 775 780

Pro Leu Asp His Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro
785 790 795

Gly Ala Arg Val Phe Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile
800 805 810

Gln Asp Ser Phe Val Glu Val Ser Pro Val Cys Pro Arg Pro Arg
815 820 825

Val Arg Leu Gly Ser Glu Ile Arg Asp Ser Val Val
830 835

<210> 254

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 254

agcccggtgca gaatcttgctc ctgg 24

<210> 255

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 255
tgaagccagg gcagcgtcct ctgg 24

<210> 256
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 256
gtacaggctg cagttggc 18

<210> 257
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 257
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 258
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
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agggcgggac gggagcccg actcgtctgc cgccgcgtc gtcgccgtcg 150

tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200
cgcccgagcc gccgctagcg cgccgcgggc atggtccctt cttaaaggcg 250
caggccgcgg cggcgggggc gggtgtgcgg aacaaagcgc cggcgcgggg 300
cctgcgggcg gctcgggggc cgcatgggc gcggcgggcc cgccgcggcg 350
gcggcgctgc ccgggcgggg cctcgcggcg cttagggcggg ctggcctccg 400
tgggcggggg cagcgggctg agggcgcgcg gagcctgcgg cggcggcg 450
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ggccggcgcg cctggctcag cgtgctgctc gggctcgcc tggcttcgt 550
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gcccacggcg ccgcgccagc cccgaggcgct gccggtcgg gcaggcggcg 650
gcttcccagg ccggcggggc gcgcggcgat gcgcgcgggg cgcaagctcg 700
gccgcggccgc tcggaccagg atggcgcccc gcgcgacagg aactttctct 750
tcgtggaggt catgaccgccc cagaaaatacc tgcagactcg ggccgtggcc 800
gcctacagaa catggtccaa gacaattcct gggaaagttc agttttctc 850
aagtgggggt tctgacacat ctgtaccaat tccagtagtg ccactacggg 900
gtgtggacga ctcctacccg ccccagaaga agtccttcat gatgctcaag 950
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tcatgacgtg tacatcaaag gagaccgtct ggagaacttc ctgaggagtt 1050
tgaacacgag cgagccccctc tttttggc agacaggctt gggaccacg 1100
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aagtggttt cttacatagg actccctttaa gattgagtt tctgaacaag 3050

atccctgttt tagctgaaga attgttattac atttgagag taaaaaaactt 4550
aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

Met Ala Ala Arg Gly Arg Arg Ala Trp Leu Ser Val Leu Leu Gly
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Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val
 245 250 255
 Gly Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser
 260 265 270
 Tyr Glu Met Arg Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys
 275 280 285
 Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala
 290 295 300
 Ile Thr Leu His Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu
 305 310 315
 His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg
 320 325 330
 Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser
 335 340 345
 Asn Thr Glu Ile His Lys Glu Asp Leu Gln Leu Gly Ile Pro Pro
 350 355 360
 Ser Phe Met Arg Phe Gln Pro Arg Gln Arg Glu Glu Ile Leu Glu
 365 370 375
 Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr Ser Ala Val Asp Gly
 380 385 390
 Gln Pro Pro Arg Arg Gly Met Asp Ser Ala Gln Arg Glu Ala Leu
 395 400 405
 Asp Asp Ile Val Met Gln Val Met Glu Met Ile Asn Ala Asn Ala
 410 415 420
 Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile Gln Tyr Gly
 425 430 435
 Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile Leu Asp
 440 445 450
 Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr Val
 455 460 465
 Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
 470 475 480
 Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys
 485 490 495
 Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser
 500 505 510
 Leu Lys Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu
 515 520 525
 His Lys Glu Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu

530	535	540
Ser Gly Arg Phe Asp Met Phe Val Arg	Phe Met Gly Asn Phe Glu	
545	550	555
Lys Thr Cys Leu Ile Pro Asn Gln Asn Val Lys	Leu Val Val Leu	
560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val Glu	
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met Gln	
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser Arg	Ala Leu Ala Leu Glu	
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu Ser	Leu Leu Phe Phe Cys	
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys Arg	
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile Phe	
650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro Ser	
665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg Asn	
680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val Arg	
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu Asp	
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr Phe	
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val Phe	
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu Gly	
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr Gln	Gln Leu Ala Glu Met	
770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn Asn	
785	790	795
Asn Gly Ser Val Arg Thr Ala		
800		

<210> 261

<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtgggc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactccgc 50
tgacaccccttc ccttcggcc ttgagggttcc cagcctggc gccccaggac 100
gttccggcgc catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttcttagt tgcgcttttgc ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacccgtga tgaagagcaa aacttgaatc attatataaca 250
agtttttagag aacccgtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaaattta aggagctgt tacacatgga gacgcttcaa ctgagaatga 400

tgtttaacc aatcctatca gtgaagaaac tacaacttc cctacaggag 450
gcitcacacc ggaaatagga aagaaaaaac acacggaaag taccccatc 500
tggtcgatca aaccaaacaa tgttccatt gtttgcatt cagaggaacc 550
ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600
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tggcattgag atctctacag aatcagaaga tgccctcag ctctcaggtg 750
aaactgcgat agaaaaaccc gaagagttt gaaagcaccc agagagttgg 800
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acaggcactt ctttgtaca ccagcaaccc agcatataga gaagatattg 900
aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950
gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000
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attctagatc taaaactctat gaatatttag atattaaatg tgccacca 1100
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atgtgttatg aacaatttc atatgcacta aaaacctaatt taaaataaaa 1400
attttggttc aggaaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
							20		25				30	

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
							35		40				45	

Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser

50	55	60
Pro Lys His Val Tyr Ser Ile Ala Ser Lys	Gly Ser Lys Phe Lys	
65	70	75
Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu		
80	85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Phe Pro Thr Gly Gly		
95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro		
110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala		
125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu		
140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val		
155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro		
170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu		
185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys		
200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp		
215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala		
230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu		
245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala		
260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro		
275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile		
290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp		
305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val		
320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala		
335	340	345

Leu Leu Lys Val Tyr
350

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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caggaatcag ttccatgtcg tggtccaccc ctacagagat gggaaagact 350
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<210> 267
<211> 466
<212> PRT
<213> Homo sapiens

<400> 267
Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val
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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

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Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu		
35	40	45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe		
50	55	60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser		
65	70	75
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp		
80	85	90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr		
95	100	105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile		
110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly		
125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile		
140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala		
155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg		
170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile		
185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu		
200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu		
215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu		
230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile		
245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp		
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys		
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys		
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro		
305	310	315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
320 325 330

Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val
335 340 345

Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp
350 355 360

Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn
365 370 375

Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr
380 385 390

Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr
395 400 405

Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe
410 415 420

Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys
425 430 435

Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr
440 445 450

Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp
455 460 465

Gly

<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 268
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tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
tgtcatttac aactgacaaa cttatgctg agttggcag agaggcttct 250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
attttataaa tctccattaa ggaaagaatt tgtcaagtct caggttatca 350
agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgc 400
agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
tgtttacat gaaaagctgc aagatgctgt aggacccct aaagtagatc 500

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ctaaaccatt gctgcggAAC acgaagaagt aaaactctag gtcagagtct 600
caggatcgTT ggtgggacag aagtagaaga gggtaatgg ccctggcagg 650
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gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaaccc 750
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aacggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
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tatgtgctgg ctccttagaa ggaaaaacag atgcatgcc gggtgactct 1150
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aataccaatc acttcatcat ttaggaagta tggaaactaa gttaaggaag 1900
tccagaaaga agccaagata tatkcttatt ttcatttcca aacaactact 1950

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caaacttcat gcaatgtact tgttctaaggc aaattaaaggc aaatatattat 2050
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cca 2103

<210> 269
<211> 423
<212> PRT
<213> Homo sapiens

<400> 269
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Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
35 40 45
Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
50 55 60
Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
65 70 75
Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
80 85 90
Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
95 100 105
Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
110 115 120
Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
125 130 135
Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
140 145 150
Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
155 160 165
Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
170 175 180
Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
185 190 195
Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
200 205 210
Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
215 220 225

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro
 230 235 240
 Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys
 245 250 255
 Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
 260 265 270
 His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser
 275 280 285
 Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp
 290 295 300
 Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly
 305 310 315
 Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg
 320 325 330
 Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro
 335 340 345
 Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly
 350 355 360
 Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly
 365 370 375
 Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly
 380 385 390
 Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly
 395 400 405
 Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys
 410 415 420

Thr Gly Ile

<210> 270
 <211> 1170
 <212> DNA
 <213> Homo sapiens

<400> 270
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gaccggccgc gcatgggaga agtgcgcatt gcggccgaag agggccgcgc 450
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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
				20					25				30	
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
				35					40				45	
Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys
				50					55				60	
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly
				65					70				75	

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
80 85 90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
95 100 105

Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
110 115 120

Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
125 130 135

Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
140 145 150

Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
155 160 165

Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
170 175 180

Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
185 190 195

Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
200 205 210

Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
215 220 225

Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
230 235

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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tgcccttggg agtaggatgt ggtgaaaagga tggggcttct cccttacggg 200
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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

Met	Ala	Arg	Glu	Asp	Ser	Val	Lys	Cys	Leu	Arg	Cys	Leu	Leu	Tyr
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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20				25						30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35				40						45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50				55						60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65				70						75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80				85						90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95				100						105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110				115						120
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
				125				130						135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
				140				145						150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
				155				160						165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser

170 175 180

Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln
185 190 195

Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met
200 205 210

Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe
215 220 225

Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu
230 235 240

Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro
245 250 255

Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His
260 265 270

Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg
275 280 285

Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe
290 295 300

Glu Met Glu Glu Leu
305

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050

aaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
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Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
20 25 30

Lys Val Gly Ile Pro Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys
 260 265 270
 Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp
 275 280 285
 Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr
 290 295 300
 Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
 305 310 315
 Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn
 320 325 330
 Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val
 335 340 345
 Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu
 350 355 360
 Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val
 365 370 375
 Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser
 380 385 390
 Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys
 395 400 405
 Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr
 410 415 420
 Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu
 425 430

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
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 ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
 ggaggcgggc aggggcccatt gcccagggtc agatactatg cagggatga 250
 acgttagggca cttagcttct tccaccagaa gggcctccag gatttgaca 300
 ctctgctcct gagtggtgat gcaaatactc tctacgtggg ggctcgagaa 350
 gccattctgg cttggatat ccagatcca ggggtccccca ggctaaagaa 400

catgataccg tggccagcca gtgacagaaa aaagagtcaa tgtgcctta 450
agaagaagag caatgagaca cagtgttca acttcatccg tgtcctggtt 500
tcttacaatg tcacccatct ctacacctgc ggcacccctcg ccttcagccc 550
tgcttgtacc ttcatattgaac ttcaagattc ctacctgttgc cccatctcg 600
aggacaaggt catggaggga aaaggccaaa gcccctttga ccccgctcac 650
aagcatacgg ctgtcttgggt ggatgggatg ctctattctg gtactatgaa 700
caacttcctg ggcagtgagc ccattctgtat gcgcacactg ggatcccagc 750
ctgtcctcaa gaccgacaac ttccctccgct ggctgcatca tgacgcctcc 800
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<210> 277
<211> 761
<212> PRT
<213> Homo sapiens

<400> 277

Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly
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Leu Phe Leu Phe Gln Leu Leu Gln Leu Leu Leu Pro Thr Thr Thr
 20 25 30

Ala Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr
 35 40 45

Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly
 50 55 60

Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr
 65 70 75

Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
 80 85 90

Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
 95 100 105

Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn
 110 115 120

Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
 125 130 135

Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala
 140 145 150

Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
 155 160 165

Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
 170 175 180

Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
 185 190 195

Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg
 200 205 210

Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg
 215 220 225

Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
 230 235 240

Gln Val Val Tyr Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
 245 250 255

Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
 260 265 270

Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
 275 280 285

Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro

290	295	300
Phe Asn Val Ile Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro	
305	310	315
Thr Ala Pro His Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val	
320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp	
335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu	
350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg	
365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr	
380	385	390
Phe Met Lys Asp His Phe Leu Met Asp	Glu Gln Val Val Gly Thr	
395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val	
410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His	Ser His Leu Val Met Tyr	
425	430	435
Leu Gly Thr Thr Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly	
440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp	
455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala	
470	475	480
Val Phe Val Gly Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala	
485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	
500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	
515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	
530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	
545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	
560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	
575	580	585

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 595 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 610 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
620 625 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 640 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 655 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
740 745 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 278

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 278

ctgctggta aatctggcgt ggag 24

<210> 279

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
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cttccgtaga agtgagcatg gctgggcagc gagtgcttct tctagtggc 100
ttccttctcc ctggggtcct gctctcagag gctgccaaaa tcctgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacggtcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttaa aaaggaagaa aaatcatatc aagtttatcag 300
ttggcttgca cctgaagatc atcaaagaga attaaaaag agtttgatt 350
tcttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcatttt taaatagaaa 450
ggatatcatg gattccttaa agaatgagaa cttcgacatg gtgatagttg 500
aaacttttga ctactgtcct ttcctgattt ctgagaagct tgggaagcca 550
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<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282
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 Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
 20 25 30
 Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
 35 40 45
 Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
 50 55 60
 Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
 65 70 75
 Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
 80 85 90
 Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
 95 100 105
 Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
 110 115 120
 Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
 125 130 135
 Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
 140 145 150
 Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile
 155 160 165
 Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro
 170 175 180
 Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met
 185 190 195
 Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
 200 205 210
 Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile
 215 220 225
 Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
 230 235 240
 Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
 245 250 255
 Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly

	260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn			
275	280	285	
Phe Ile Ala Lys Phe Gly Asp Ser Gly Phe Val Leu Val Thr Leu			
290	295	300	
Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu			
305	310	315	
Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val Ile Trp Lys			
320	325	330	
Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala Ala Asn			
335	340	345	
Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala His			
350	355	360	
Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile			
365	370	375	
Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu			
380	385	390	
Phe Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys			
395	400	405	
Phe Gly Val Ser Ile Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu			
410	415	420	
Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser			
425	430	435	
Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser			
440	445	450	
Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr			
455	460	465	
Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp			
470	475	480	
His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu			
485	490	495	
Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala			
500	505	510	
Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr			
515	520		

<210> 283

<211> 24

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 283
tgccttgct cacctacccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
tcaggctggt ctccaaagag aggg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 285
cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
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cccgtcacac acacatacca tgttctccat ccccccaagg ccagccctca 150
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250
tgctgtcact gcatgctctg ccaaggagga gggaaactgca gtgacagcag 300
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ccagggagag gagcggaaac agaagagggg cagaagaccg gggacttgt 450

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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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		20						25				30		
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
		35						40				45		
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
		50						55				60		
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
		65						70				75		
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80				85				90		
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100				105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115				120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125				130				135		
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140				145				150		
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160			165		
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

170 175 180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser
185 190 195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu
200 205

<210> 288
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 288
aggcagccac cagctctgtg ctac 24

<210> 289
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 289
cagagaggga agatgaggaa gccagag 27

<210> 290
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-42
<223> Synthetic construct.

<400> 290
ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291
<211> 1570
<212> DNA
<213> Homo sapiens

<400> 291
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tagccgcccc gcctcgacgc cgtcccgaaa cccctgtgct ctgcgcgaag 100
ccctggcccc gggggccggg gcatggcca ggggcgcggg gtgaagcggc 150

ttcccgcccc gccgtgactg ggcgggcttc agccatgaag accctcatag 200
ccgcctactc cggggtcctg cgccggcggc gtcaggccga ggctgaccgg 250
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<210> 292
<211> 388
<212> PRT
<213> Homo sapiens

<400> 292
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Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro
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Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
35 40 45
Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
50 55 60
Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
65 70 75
Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
80 85 90
Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
95 100 105
Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
110 115 120
Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
125 130 135
Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
140 145 150
Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
155 160 165
Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
170 175 180
Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu
185 190 195
Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
200 205 210
Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu
215 220 225
Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Val Val Gly Gly
230 235 240
Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr
245 250 255
Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly

260 265 270

Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr
275 280 285

Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln
290 295 300

Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His
305 310 315

Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr
320 325 330

Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro
335 340 345

Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr
350 355 360

Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr
365 370 375

Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn
380 385

<210> 293
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 293
gctgacctgg ttcccatctta ctcc 24

<210> 294
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 294
cccacagaca cccatgacac ttcc 24

<210> 295
<211> 50
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggaggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
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cggggccgcg gaggcgacgc cggggacgcc cgcgacgca gcaggtggcg 150
gcggctgcag ctgttgcag ccgaaagccc tgagggcagc tgttccact 200
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cagctctacc gcccgcctcaa ctgcccgcctc gcctactcac tctggagcca 450
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accctgtctc 3060

<210> 297
<211> 368
<212> PRT
<213> Homo sapiens

<400> 297
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
1 5 10 15
Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
20 25 30
Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
35 40 45
Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
50 55 60
Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
65 70 75
Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
80 85 90
Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
95 100 105
Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
110 115 120
Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
125 130 135
Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
140 145 150
Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
155 160 165

Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe
 170 175 180
 Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys
 185 190 195
 Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly
 200 205 210
 Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val
 215 220 225
 Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
 230 235 240
 Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
 245 250 255
 Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala
 260 265 270
 Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln
 275 280 285
 Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys
 290 295 300
 Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala
 305 310 315
 Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe
 320 325 330
 Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val
 335 340 345
 Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu
 350 355 360
 Glu Pro Gly Arg Trp Arg Leu Gln
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<210> 298
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 298
 cttcctctgt gggtggacca tgtg 24

<210> 299
 <211> 21
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggcctt cgctaagaag gagctgctct acgtccccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tgtcctgggg cagccaccag gcatattcat ctttgtgt gtttttcttt 100

tgcttagca ctggggact tctgcttat ttctttggta ggaaagggc 150

tcagttgtc ttgtggggtt ggtggcaggc aggccggctt acgcctgata 200

cggccctggg ttagaaggga aggaagata aactttata caaatggga 250

tagctgggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300

ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcaggc 350

ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgcccccctg gccagttca ttgtacatgt ggtgttctct 450

tgtcgccct gtaatgtggt atgccatggg gtcttgcac aagccttcc 500

tcttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550

atgtagtcatt cctgcagatt tcaattctaa catcatttc tccagggatc 600

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gcggaggttg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300
acagagttag actctatgtc caaaaaaaaaaaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile
1 5 10 15

His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe
20 25 30

Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly
35 40 45

Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val
50 55 60

Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp
65 70 75

Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr
80 85 90

Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln
95 100 105

Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu
110 115 120

Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr
125 130 135

Cys Gly Val Leu Leu Ser Phe Leu

<210> 303
<211> 1768
<212> DNA
<213> Homo sapiens

<400> 303
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gaggccgagg cggttagatc acctgaggtc aggagttcaa gaccagcctg 1550
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gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
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<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

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Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20				25				30		
Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35				40				45		
Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50				55				60		
Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
				65				70				75		
Thr	Val	Ser	Arg	Leu	Glu	Ala	Leu	Thr	Arg	Ala	Val	Gln	Val	Ala
				80				85				90		
Glu	Pro	Leu	Gly	Ser	Cys	Gly	Phe	Gln	Gly	Gly	Pro	Cys	Pro	Gly
				95				100				105		
Arg	Arg	Arg	Asp											

<210> 305

<211> 989

<212> DNA

<213> Homo sapiens

<400> 305

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ccgccttcgc cactggcctc ttcatggga ggccgtgccc cccatggcga 200
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cggcgaggc tcagggctta catcagccctc ctggccctgg gcgatggact 850
caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900
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ataaaagtggg gctggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
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Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
					20				25				30	
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35				40				45		
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50				55				60		

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
 65 70 75
 Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
 80 85 90
 Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
 95 100 105
 Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
 110 115 120
 Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
 125 130 135
 Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
 140 145 150
 Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
 155 160 165
 Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
 170 175 180
 Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
 185 190 195
 Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
 200 205 210
 Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
 215 220 225
 Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
 230 235 240
 Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
 245 250 255
 Leu Thr Leu Ala Phe Lys Ile
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<210> 307
 <211> 2272
 <212> DNA
 <213> Homo sapiens

<400> 307
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 gctaagatga agggctaccc tcactggctt gccaggatcg acgacatcgc 150
 ggatggcgcc gtgaagcccc cacccaacaa gtacccatc ttttctttg 200
 gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

ESTATE REPORT

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aggcgtgtgg gagatccaga acaacccca cgccagctac agcgcccctc 350
cgccagttagt ctcctccgac agcgaggccc ccgaggccaa ccccgccgac 400
ggcagtgacg ctgacgagga cgatgaggac cggggggta tggccgtcac 450
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gtcagcctcc gactccgact ccaaggccga ttccggacggg gccaagcctg 800
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tcaagtcgcg ggtcctcgcc ccaaagatcg aggccgtgca gaaagtgaac 1750
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actataaacg gtttttaat ga 2272

<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met Pro His Ala Phe Lys Pro Gly Asp Leu Val Phe Ala Lys Met
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Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Asp Ile Ala Asp
20 25 30

Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe
35 40 45

Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
50 55 60

Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
65 70 75

Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
80 85 90

Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
95 100 105

Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
110 115 120

Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
125 130 135

Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Lys Ser Ser

140	145	150
Asp Asn Ser Gly Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met Ser	
155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln Ala	
170	175	180
Ser Val Ser Pro Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser Glu	
185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys Ala	
200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys Lys	
215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp Ser	
230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala	Met Ala Arg Ser Ala Ser	
245	250	255
Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp	Val Ser Val Ser Val	
260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu Pro	
275	280	285
Lys Pro Arg Gly Arg Lys Pro Glu Arg	Pro Pro Ser Ser	
290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser Glu	
305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg	Glu Leu Glu Ala Arg	
320	325	330
Arg Arg Arg Glu Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu Gln	
335	340	345
Glu Lys Glu Glu Lys Glu Arg Arg Glu	Arg Ala Asp Arg Gly	
350	355	360
Glu Ala Glu Arg Gly Ser Gly Ser Ser	Gly Asp Glu Leu Arg	
365	370	375
Glu Asp Asp Glu Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg Gly	
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu Leu	
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser Ser	
410	415	420
Thr Glu Pro Ala Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val Arg	
425	430	435

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
 440 445 450
 Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
 455 460 465
 Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
 470 475 480
 Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
 485 490 495
 Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
 500 505 510
 Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
 515 520 525
 Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
 530 535 540
 Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
 545 550 555
 Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
 560 565 570
 Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
 575 580 585
 Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
 590 595 600
 Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
 605 610 615
 Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
 620 625 630
 Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
 635 640 645
 Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala
 650 655 660
 Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser
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<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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<210> 310
<211> 777
<212> PRT
<213> Homo sapiens

<400> 310
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Phe His Leu Phe Pro Ala Leu Met Met Leu Ser Met Thr Met Leu
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Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu
35 40 45
Lys Leu Thr Tyr Lys Asp Leu Leu Ser Asn Ser Cys Ile Pro
50 55 60
Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
65 70 75
Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80	85	90
Phe Leu Leu Ser	Leu Val Asp	Leu Asn Lys
95	100	105
Tyr Trp Pro Ala Ala	Lys Glu Arg Val	Glu Leu Cys Lys
110	115	120
Gly Lys Asp Ala Asn	Thr Glu Cys Ala Asn	Phe Ile Arg Val
125	130	135
Gln Pro Tyr Asn Lys	Thr His Ile Tyr Val	Cys Gly Thr Gly Ala
140	145	150
Phe His Pro Ile Cys	Gly Tyr Ile Asp	Leu Gly Val Tyr Lys
155	160	165
Asp Ile Ile Phe Lys	Leu Asp Thr His	Asn Leu Glu Ser Gly Arg
170	175	180
Leu Lys Cys Pro Phe	Asp Pro Gln Gln	Pro Phe Ala Ser Val
185	190	195
Thr Asp Glu Tyr Leu	Tyr Ser Gly Thr	Ala Ser Asp Phe Leu
200	205	210
Lys Asp Thr Ala Phe	Thr Arg Ser Leu	Gly Pro Thr His Asp
215	220	225
His Tyr Ile Arg Thr	Asp Ile Ser Glu	His Tyr Trp Leu Asn
230	235	240
Ala Lys Phe Ile Gly	Thr Phe Phe Ile	Pro Asp Thr Tyr Asn
245	250	255
Asp Asp Asp Lys Ile	Tyr Phe Phe	Arg Glu Ser Ser Gln
260	265	270
Gly Ser Thr Ser Asp	Lys Thr Ile Leu	Ser Arg Val Gly Arg
275	280	285
Cys Lys Asn Asp Val	Gly Gly Gln Arg	Ser Leu Ile Asn Lys
290	295	300
Thr Thr Phe Leu Lys	Ala Arg Leu Ile	Cys Ser Ile Pro Gly
305	310	315
Asp Gly Ala Asp Thr	Tyr Phe Asp Glu	Leu Gln Asp Ile Tyr
320	325	330
Leu Pro Thr Arg Asp	Glu Arg Asn Pro	Val Val Tyr Gly Val
335	340	345
Thr Thr Thr Ser Ser	Ile Phe Lys Gly	Ser Ala Val Cys Val
350	355	360
Ser Met Ala Asp Ile	Arg Ala Val Phe	Asn Gly Pro Tyr Ala
365	370	375

Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile
 380 385 390
 Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro
 395 400 405
 Leu Ile Lys Ser Thr Arg Asp Phe Pro Asp Asp Val Ile Ser Phe
 410 415 420
 Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala
 425 430 435
 Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr
 440 445 450
 Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp
 455 460 465
 Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val
 470 475 480
 Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu
 485 490 495
 Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu
 500 505 510
 Leu Ser Leu Lys Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly
 515 520 525
 Leu Val Gln Leu Ser Leu His Arg Cys Asp Thr Tyr Gly Lys Ala
 530 535 540
 Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp
 545 550 555
 Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala
 560 565 570
 Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp
 575 580 585
 Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val
 590 595 600
 Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro
 605 610 615
 Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly
 620 625 630
 Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys
 635 640 645
 Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser
 650 655 660
 Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr

665 670 675
Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu
680 685 690
Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu
695 700 705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu
710 715 720
Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp
725 730 735
His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp
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Lys His Met Gln Glu Met Lys Lys Arg Asn Arg Arg His His
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Arg Asp Leu Asp Glu Leu Pro Arg Ala Val Ala Thr
770 775

<210> 311
<211> 25
<212> DNA
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<222> 1-25
<223> Synthetic construct.

<400> 311
caacgcagcc gtgataaaca agtgg 25

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<213> Artificial

<220>
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<222> 1-24
<223> Synthetic construct.

<400> 312
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<210> 313
<211> 45
<212> DNA
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<220>
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<222> 1-45
<223> Synthetic construct.

<400> 313
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<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

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<210> 315
<211> 370
<212> PRT
<213> Homo sapiens

<400> 315
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Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala
							35			40				45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg
							50			55				60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu
							65			70				75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala
							80			85				90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser
							95			100				105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp
							110			115				120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu
							125			130				135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro
							140			145				150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp
							155			160				165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu
							170			175				180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu
							185			190				195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser
							200			205				210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu
							215			220				225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln
							230			235				240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu
							245			250				255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly
							260			265				270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu
							275			280				285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu
							290			295				300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala

305 310 315
Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly
320 325 330
Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro
335 340 345
Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Pro Ala Lys Ala
350 355 360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr
365 370

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<211> 4407
<212> DNA
<213> Homo sapiens

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<210> 317
<211> 837
<212> PRT
<213> Homo sapiens

<400> 317
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35 40 45
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

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Gly Val Leu Gln Tyr Arg Gly Ala Glu	Leu His Leu Gln Pro	Leu
155	160	165
Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His	Ile
170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys	Asn
185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg	Ala
200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val	Val
215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys	Arg
230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Lys Ala Phe Lys	His
245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu	Val
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser	Ala
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu	Asn
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile	Leu
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr	Leu
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser	Cys
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala	Ala
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser	Lys
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His	Val
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp	Ser
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly	Tyr
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu	Pro
425	430	435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln
 440 445 450
 Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro
 455 460 465
 Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
 470 475 480
 Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys
 485 490 495
 Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp
 500 505 510
 Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro
 515 520 525
 Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val
 530 535 540
 Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly
 545 550 555
 Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn
 560 565 570
 Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu
 575 580 585
 Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe
 590 595 600
 Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro
 605 610 615
 Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr
 620 625 630
 Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser
 635 640 645
 Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
 650 655 660
 Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys
 665 670 675
 Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly
 680 685 690
 Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile
 695 700 705
 Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
 710 715 720
 Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

725 730 735

Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp
740 745 750

Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr
755 760 765

Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro
770 775 780

Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg
785 790 795

Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro
800 805 810

Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu
815 820 825

Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys
830 835

<210> 318
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 319
 ctgtgctttt cggtgcagcc agtc 24

<210> 320
<211> 43
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-43
<223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct gggcagtca gttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
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ttgtggactg gtgttggtta tcctggccct aactctaatt gtccctgttt 200
gggggagcaa gcacttctgg ccggaggtac ccaaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggactgtatg 350
aacatttggaa agtgcacgac tttaaaaacg gatacactgg catctacttc 400
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attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttcttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
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<210> 322

<211> 317
<212> PRT
<213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	
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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
				20					25						30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
				35					40						45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
				50					55						60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
				65					70						75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
				80					85						90
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
				95					100						105
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
				110					115						120
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
				125					130						135
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
				140					145						150
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
				155					160						165
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
				170					175						180
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
				185					190						195
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
				200					205						210
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
				215					220						225
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
				230					235						240
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
				245					250						255
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
				260					265						270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ggccgtgcag cttctggct tcctgctcag cttcctggc atggtggca 150
cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtggc 200
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gtttggtcag tggggtttgtt gtgtatcca ggaataaaacc ttgcggatgt 1150
ggctgtttat gaaaaaaaaaaa aaaa 1174

<210> 324
<211> 239
<212> PRT
<213> Homo sapiens

<400> 324
Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe
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Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
20 25 30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
35 40 45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
50 55 60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
65 70 75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
80 85 90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
95 100 105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
110 115 120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
125 130 135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
140 145 150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
155 160 165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
170 175 180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
185 190 195
Ala Pro Pro Arg Ala Thr Thr Thr Ala Asn Thr Ala Pro Ala
200 205 210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
230 235

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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gcatcgccgc caccggatg gacatgtgga gcacccagga cctgtacgac 200
aaccccgta cctccgtt ccagtacgaa gggctctgga ggagctgcgt 250
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gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcata 350
gtcctgggtg ccattggcct cctggtatcc atcttgccc tgaaatgcat 400
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aggtaaaac taattctta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
1														15

Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
														30

Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
														45

Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
														60

Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
														75

Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg		
95	100	105
Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr		
110	115	120
Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly		
125	130	135
Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser		
140	145	150
Thr Ala Asn Met Tyr Thr Gly Met Gly Gly Met Val Gln Thr Val		
155	160	165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val		
170	175	180
Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala		
185	190	195
Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser		
200	205	210
Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe		
215	220	225
Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile		
230	235	240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro		
245	250	255
Ser Lys His Asp Tyr Val		
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<210> 327

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

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tgaattgcgt gaggcaggct aacatcgagg tgcaagtcaa aatctatgtat 300
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ccctgtgagc tgggtgccca atgccatcat cagagattc tataactcaa 550
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ttttctaatt 2010

<210> 328
<211> 225
<212> PRT
<213> Homo sapiens

<400> 328
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Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
20 25 30
Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
35 40 45
Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
50 55 60
Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
65 70 75
Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
80 85 90
Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
95 100 105
Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
110 115 120
Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
125 130 135
Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
140 145 150
Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
155 160 165
Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
170 175 180
Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
185 190 195
Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
200 205 210

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
215 220 225

<210> 329

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

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cagctatgtaa gaccccccggcc cccacctccaa acactgcacc cttctgccc 1250

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tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu
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Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp
20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135

Val Cys Trp Thr Ala His Ala Ile Arg Asp Phe Tyr Asn Pro
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Gly Gly Gly Leu
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
185 190 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
215 220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

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ccaaagcata ccttctggaa acttcaggag tccttcatttc cctgacgggt 500
atcttcgttc tgattccggc gagctggaca gccaatataa tcattcagaga 550
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cactttcct tggctggca agcgctgctg tccttcatttc tggaggggt 650
ctgctttgtg gattttgtc ctgcaacaga aagaagcaag ggtacagata 700
tccagtgccct ggctaccgtg tgccacacac agataagcga agaaatacga 750
caatgcttag taagacctcc accagttatg tctaattgcct cttttggct 800
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taagtatgtg aggcaaggaga acttgctta tgtcttagatt tacattgata 900
cgaaagtttc aatttgttac tgggtggtagg aatgaaaatg acttacttgg 950
acattctgac ttcagggtgtt ttaaatgcat tgactattgt tggaccata 1000
cgctgctcca attttcatat tctaaattca agtataccca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
ctgataagaa tctaaagttt aaattgatat tctataacaa taaaacatat 1150
acctattctta 1160

<210> 332
<211> 173
<212> PRT
<213> Homo sapiens

<400> 332
Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

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1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg			
20	25		30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu			
35	40		45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn			
50	55		60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe			
65	70		75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala			
80	85		90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly			
95	100		105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser			
110	115		120
Ala Ala Val Leu Phe Ile Gly Gly Leu Leu Cys Gly Phe Cys			
125	130		135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly			
140	145		150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu			
155	160		165
Ser Lys Thr Ser Thr Ser Tyr Val			
170			

<210> 333
<211> 535
<212> DNA
<213> Homo sapiens

<400> 333
agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
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ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
agaagtatcc agtggtgccc atcccctgcc ccatcacata cctaccagg 200
tgtggttctg actacatcac ctatggaat gaatgtcaact tgtgtaccga 250
gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
tcatcatcccc aggctctgac tgagttctt tcagtttac tgatgttctg 400
ggtgaaaaac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcatttt 500
ttttaaacac gtcaataaaa aaataatctc ccaga 535

<210> 334
<211> 85
<212> PRT
<213> Homo sapiens

<400> 334
Met Lys Ile Thr Gly Gly Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15
Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30
Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60
Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75
Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335
<211> 742
<212> DNA
<213> Homo sapiens

<400> 335
cccgccccg gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50
ctgctcgccgc cccggcccca tggctgcctc ccccgccgg cctgctgtcc 100
tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150
ggcataagtg gaaataaaact caagctgatg cttaaaaaac gagaagcacc 200
tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250
tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300
cccgagggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350
agcgaaattt gaagatgaca tcacctattt gcttaacaga gatcgaaatg 400
gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450
gcaattggtc cccggagccc ctacggcttt aggcatggag ccagcgtcaa 500
ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550
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tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaaa 650
gaagagttaa aacaacacat gtaaatgcct tttgatattt catggaaatg 700
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
1 5 10 15
Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337
cggtcgagc ccggccggaa gtggccgagg ggccgcgatg gagctgggg 50
agccgggcgc tcggtagcgc ggcggcaag gcaggcgcca tgaccctgat 100
tgaagggtg ggtgatgagg tgaccgtcct tttctcggtg ctgcctgcc 150
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
gaccactgc cccagccgtc agggacccc acgccatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggccccca gggcagaga 300
cccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacf 350
gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcg 400
gctacggctg aaattcctca atgattcaga gcaggtggcc agggctggc 450
cccacgacac cattggctcc ttgaaaagga cccagttcc cgccgggaa 500
cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacaccca 550
gaccctgggc agcattcacc tccctccaa ctgcgttctc cactgccacg 600
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cccgccccct ccgggctgga aatcgccagc ctgctgctgc ccctgctgct 700
cctgctgttg ctgctgctct ggtactgcca gatccagtag cggcccttct 750
ttccctgac cgccactctg ggcctggccg gttcacccct gtcctcagt 800
ctcctggcct ttgccatgta ccgccccgtag tgcctcccgcc ggccgttggc 850
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cgcaactggga gtgggctcct cggggctcgcc catctgctgt cgctgcctcg 1100
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gttccccggaa acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaaa 1300
aaaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
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Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25				30	

Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35				40				45		

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
 50 55 60
 Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
 65 70 75
 His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
 80 85 90
 Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
 95 100 105
 Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
 110 115 120
 Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
 125 130 135
 Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
 140 145 150
 Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
 155 160 165
 Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
 170 175 180
 Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
 185 190 195
 Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu
 200 205 210
 Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
 215 220 225
 Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
 230 235 240
 Phe Ala Met Tyr Arg Pro
 245

<210> 339
 <211> 849
 <212> DNA
 <213> Homo sapiens

<400> 339
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 caagacccta agaaccatca gccctcagct gcacccctc ccctccaagg 150
 atgacaaagg cgctactcat ctatggtc agcagcttc ttgccctaaa 200
 tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgga tgggttgag ggtaactccc tgagtgactg gctgtgcctg 300
gctttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
tggaaagctt gactatggcc tcttcagat caacagccac tactggtgca 400
acgattataa gagttactcg gaaaacctt gccacgtaga ctgtcaagat 450
ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
gtccggagca cggggatga acaactgggt agaatggagg ttgcactgtt 550
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
agggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
ggattttca tttttttttc ctactgcctc cacttcatgt tatttttttc 700
ccttcccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750
tcttggcttc ctccttactc ccacatctggac ccagtccttc ggttcctgtc 800
tgttatgtt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
1 5 10 15

Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val
20 25 30

Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
35 40 45

Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
50 55 60

Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
65 70 75

Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
80 85 90

Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
95 100 105

Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
110 115 120

Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
125 130 135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ccctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcatcctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50
actgagaacc caccagctca tcccagacac ctcatalogaa cctatttata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatta ttttttccc 150
aaggagaaaa ccggggtaaa gggagggaaag caattcaatt tgaagtccct 200
gtgaatgggc ttccagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggtttctg attgttaagtg gaagcaggc 300
ttgcacacgc ttttggcaaa tgtcaggacc aggttaagtg actggcagaa 350
aaacttccag gtggacaacaag caacccatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaagct aacttgaaca tgacctgttgcatttggcaa 450
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
ctccagttcc tcctgctgtc cctgatgttg ggatgcgtcc tggatgttgtt 550
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ESTIMATE

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tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
1 5 10 15

Phe Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Gly Ser Tyr Arg Leu Ile
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly
 260 265 270
 Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His
 275 280 285
 Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile
 290 295 300
 Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile
 305 310 315
 Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg
 320 325 330
 Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro
 335 340 345
 Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg
 350 355 360
 Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr
 365 370 375
 Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly
 380 385 390
 Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly
 395 400 405
 Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln
 410 415 420
 Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg
 425 430 435
 Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu
 440 445 450
 Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala
 455 460 465
 Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu
 470 475 480
 Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu
 485 490 495
 Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His
 500 505 510
 Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp
 515 520 525
 Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg
 530 535 540
 Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe

545 550 555
Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val
560 565 570
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln
575 580 585
His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser
590 595 600
Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu
605 610 615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe
620 625 630
Asp Gln Ile Asn Ala Val Asp Glu Arg
635

<210> 348
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 348
ggagaggtgg tggccatgga cag 23

<210> 349
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 349
ctgtcactgc aaggagccaa cacc 24

<210> 350
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 350
tatgtcgctg cgaggtggtg aaaacctcga actgtcttgc aaggc 45

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
cgccaagcat gcagtaaagg ctgaaaatct gggcacacgc tgaggaagac 50
ctcagacatg gagtccagga tgtggctgc gctgctgctg tcccacacctcc 100
tccctctctg gccactgctg ttgctgcccc tcccacccgcc tgctcagggc 150
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccggtgtgc 200
caggggaggc ccctcgcccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtccctg 300
cctggcactg caccggcagc cacccatca ggcttgagg agggccgccc 350
ctcatcccaa taccctggg ctatcgtgtg gggtcccacc gtgtctcgag 400
aggatggagg ggacccaaac tctgccaatc ccggatttct ggactatgg 450
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1					5				10				15	

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 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
 140 145 150
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
 155 160 165
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
 170 175 180
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
 185 190 195
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
 200 205 210
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
 215 220 225
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 230 235 240

Leu Pro Lys

<210> 353
 <211> 480
 <212> DNA
 <213> Homo sapiens

<400> 353
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gccccccaccc tcgcGCCAGG acccgaggac agcaccgcgc aggagcggct 300
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gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
1				5				10					15	

Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu
				20				25					30	

Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35				40					45	

Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50				55					60	

Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65				70					75	

Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Ser	Leu	Gly	Pro	
				80				85					90	

Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
				95				100					105	

Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
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Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala
1					5				10					15

His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser
					20				25					30

Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp
					35				40					45

Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr
					50				55					60

Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu
					65					70				75

Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln
					80				85					90

Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu
					95				100					105

Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala
					110				115					120

Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gln	
					125				130					135

Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	
1								5		10				15	
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	
								20		25				30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	
								35		40				45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	
								50		55				60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	
								65		70				75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	
								80		85				90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	
								95		100				105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	
								110		115				120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	
								125		130				135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	
								140		145				150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	
								155		160				165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	
								170		175				180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	
								185		190				195	

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
200 205 210

Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225

Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255

Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270

Val Glu Leu

<210> 359
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 359
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<210> 360
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 360
tgacgagtgg gatacactgc 20

<210> 361
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 361
gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
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<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
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卷之三

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<210> 364
<211> 269
<212> PRT
<213> Homo sapiens

<400> 364
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Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
    20          25          30

Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
    35          40          45

Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
    50          55          60

Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
    65          70          75

Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
    80          85          90

Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
    95         100         105

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Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile
 110 115 120
 Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys
 125 130 135
 Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile
 140 145 150
 Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val
 155 160 165
 Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr
 170 175 180
 Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn
 185 190 195
 Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser
 200 205 210
 Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly
 215 220 225
 Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile
 230 235 240
 Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile
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 Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn
 260 265

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
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 gcctctggcc gagccgccac aggagcagtc cctcgccccc tggctccgc 300
 agaccccgcc gccgcctgc tccaggtct tcgccagagc catcgagagc 350
 agccgcgacc tgctgcacag gatcaaggat gaggtggcg cacccggcat 400
 agtggttgga gtttctgttag atggaaaaga agtctggta gaaggtttag 450
 gttatgctga tggtgagaac cgttaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
gtggaaagca gggaaactgg atcttgatata tccagtacaa cattatgttc 600
ccgaattccc agaaaaagaa tatgaaggtaaaaaggttgc tgtcacaaca 650
agattactga tttcccattt aagtggatt cgtcattatg aaaaggacat 700
aaaaaaaggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
agaatgtgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
gattttacta aatttaaaac agagcaggag aatgaaggcca aatgccgaa 850
ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900
tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt attaaaaat 950
gatccttgc tcttcaaacc tgtagtcag ttttgtatt caactttgg 1000
ctatacccta ctggcagccca tagtagagag agcttcagga tgtaaatatt 1050
tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
caggaagaaa acgagccagt gattacaat agagcaaggt aaatgaatac 1150
cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200
aagtcaaatt ttcttgaaaat ccattccaaa atcaacctgc cacattttgg 1250
gagctttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300
catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1														15
Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
														30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
														45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
														60
Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu
														75
Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro
														90
80														
85														

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala
 95 100 105
 Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp
 110 115 120
 Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly
 125 130 135
 Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn
 140 145 150
 Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile
 155 160 165
 Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala
 170 175 180
 Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu
 185 190 195
 Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr
 200 205 210
 Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys
 215 220 225
 Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys
 230 235 240
 Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys
 245 250 255
 Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu
 260 265 270
 Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn
 275 280 285
 Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn
 290 295 300
 Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe
 305 310 315
 Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu
 320 325 330
 Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
 335 340 345
 Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
 350 355 360
 Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
 365 370

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaaaagaa gtctggtcag aaggtttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggctt cattctccctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacacctcag aacaactcat tttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgcttt gccaaattgt ggaaaggcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggc gggagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgtcttgc tcatggcggt agcagcgccc 150
agtgcggccc gggcagcgg ctgccggcc gggactggtg cgcgaggggc 200
tggggcggaa ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250
tggagcactc attttagatc gatgacagtgc ccaacttccg gaagcggggc 300
tcactgctct ggaaccagca ggttgttacc ttgtccctgt cacagcggca 350
gctcagcggag gaggagcggg gccgactccg ggtgtggca gccctgaatg 400
gcctgttaccg ggtccggatc ccaaggcgac ccggggccct ggttgttacc 450
gaagctggtg gctatgttctc ctccttgc cctgcgtgtt ccctggtgta 500
gtcgacccctg tcggaccaggc tgaccctgca cgtggatgtg gccggcaacg 550
tgggtggcggt gtcgggtggtg acgcaccccg gggctgccc gggccatgag 600
gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650
gccaccaca gccccaggcc ctgagacggc ggcatttattt gagcgcctgg 700
agatgaaaca gccccagaag gccaagaacc cccaggagca gaagtccttc 750
ttcgccaaat actggatgtt catcattccc gtcgttccgtt tcctcatgtat 800
gtcaggagcg ccagacacccg gggccaggg tgggggtggg ggtgggggtg 850
gtgggtgggg tagtggccctt tgctgtgtgc caccctccct gtaagtctat 900
ttaaaaacat cgacgataca ttgaaatgtt tgaacgtttt gaaaagctac 950
agcttccagc agccaaaagc aactgttggt ttggcaagac ggtcctgtat 1000
tacaagcttggt attgaaattt actgctcaact tgatacgtt ttcagaaacc 1050
caaggaatgg ctgtccccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
ttgtgtggca gtttattttt ctgtccccca gatcgacacg caaaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu
1								10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
	20							25					30	

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
			35					40					45	

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
 50 55 60
 Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
 65 70 75
 Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
 80 85 90
 Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
 95 100 105
 Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
 110 115 120
 Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
 125 130 135
 Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
 140 145 150
 Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
 155 160 165
 Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
 170 175 180
 Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
 185 190 195
 Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
 200 205 210
 Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
 215 220 225
 Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
 230 235 240
 Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly
 245 250 255
 Gly Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
 260 265

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgctgc tggAACCGA gcccggccg gagccacagc ggggagggtg 50
 gcctggcgcc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100
 cagcaggtcg tccggggggcc caccatgctg gtgactgcct accttgcttt 150
 tgttaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctaaacccccc tggaagggcc tgcagcaatc ctccttcct tcggttcaa 250
ctggacttct atcaggctta ctccctggcc ctggcagctg attggctca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
cctottctcc ctgacttact cactatgctg cttAACAAA ctctctcaag 500
actacttgt gctgcttagtg gggcgagcac ttggggct gtccacagcc 550
ctgctttct cagccttcga ggcctggat atccatgagc acgtggaacg 600
gcatgacttc cctgctgagt ggatcccagc taccttgct cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgttagcg ccctttgtgg ctgccatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accggccgcgt gctgctgctg ggcaccatac aagctctatt 900
tgagagtgtc atcttcatct ttgtttctt ctggacacct gtgctggacc 950
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
tcagccccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
tcttcatgtt gacttctct accagcccag gccaggagag tccggtgag 1150
tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
cagcatgagc ttccctacgga gaaagggtgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctggttccgg gtacctctgc actcaactggc ttgccttaggg 1300
ctccttgc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tggtgatggc tctgctggca gtggggac 1400
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacacct 1450
gaggaggccct atgcccctga gctgtAACCC cactccagga caagatagct 1500
gggacagact cttgaattcc agctatccgg gattgtacag atctctgtgt 1550
gactgacttt gtgactgtcc tgtggttct cctgcccattt ctgtgtttt 1600
gggaggacat gatgggggtg atggactgga aagaagggtgc caaaagttcc 1650

ctctgtgtta ctcccatatta gaaaataaac acttttaaat gatcaaaaaa 1700
aaaaaa 1706

<210> 374
<211> 450
<212> PRT
<213> Homo sapiens

<400> 374
Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
1 5 10 15
Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30
Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45
Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
50 55 60
Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75
Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90
Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105
Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120
Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135
Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150
Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
155 160 165
Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180
Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
185 190 195
Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
200 205 210
Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
215 220 225
Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
230 235 240

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile
 245 250 255
 Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp
 260 265 270
 Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe
 275 280 285
 Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg
 290 295 300
 Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu
 305 310 315
 Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr
 320 325 330
 Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile
 335 340 345
 Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser
 350 355 360
 Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala
 365 370 375
 Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys
 380 385 390
 Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr
 395 400 405
 Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu
 410 415 420
 Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu
 425 430 435
 Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu
 440 445 450

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

gcgacgcgca gccccccggc gagaggaaac gcggcgccgg gccggcccg 50

gcccggaga tggccccgg cggcgccgg tggtgttgc tcgtgctctg 100

gctccccggc tgctcgccg cccacggctt ccgtatccat gattatttgt 150

actttcaagt gctgagtcct gggacattc gatacatctt cacagccaca 200

cctgccaagg actttggtgg tatcttcac acaaggatg agcagattca 250

ccttgtcccc gctgaacctc cagaggcctg cggggactc agcaacgggtt 300
tcttcatcca ggaccagatt gctctgggtgg agaggggggg ctgctcccttc 350
ctctccaaga ctcgggtggt ccaggagcac ggcgggcggg cggtgatcat 400
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
acagtaccca ggcacagct gacatccccg ccctttcct gctcgccga 500
gacggctaca tggatccggcc ctctctggaa cagcatgggc tgccatgggc 550
catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
tgcaaccgcc ctggacccctc tggtagaaga gtttgcctca cattccagcc 650
ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
tttggcggt gctaggctga aagggaagcc acaccactgg ccttcccttc 800
cccgaggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
ccccagggtct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
tacccagggt ctctgcacag tgacccctcac agcagttgtt ggagtggttt 1000
aaagagctgg tgtttgggaa ctcaataaac cctcactgac ttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1								10						15
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20					25						30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
									35					45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
				50					55					60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
				65					70					75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
					80				85					90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
95 100 105

Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
110 115 120

Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
125 130 135

Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
140 145 150

Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
155 160 165

Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
170 175 180

Leu Gln Pro Pro Trp Thr Phe Trp
185

<210> 377

<211> 496

<212> DNA

<213> Artificial

<220>

<221> unsure

<222> 396

<223> unknown base

<400> 377

tctgcctcca ctgctctgtg ctggatcat ggaacttgca ctgctgtgtg 50

ggctgggtgt gatggctgggt gtgattccaa tccagggcgg gatcctgaac 100

ctgaacaaga tggtaagca agtgaactggg aaaatgccc tccttccta 150

ctggccctac ggctgtcaact gcggacttagg tggcagaggc caacccaaag 200

atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250

aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300

ttgtatggat ttatctcaac gctattgttt aatggctgtg ttatgtga 350

tctatctgga aaatgaggac tccgaataaa aagctattac tawtnaaaa 400

aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 450

aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
1 5 10 15

Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
20 25 30

Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
35 40 45

Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
50 55 60

Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
65 70 75

Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
80 85 90

His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
95 100 105

Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
110 115

<210> 379
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 379
ctgcctccac tgctctgtgc tggg 24

<210> 380
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 380
cagagcagtg gatgttcccc tggg 24

<210> 381
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45

<223> Synthetic construct.

<400> 381
ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctc 45

<210> 382
<211> 764
<212> DNA
<213> Homo sapiens

<400> 382
ctcgcttctt ccttctggat gggggcccgag ggggcccagg agagtataaa 50
ggcgatgtgg agggtgcggc gcacaaccag acgcccagtc acaggcgaga 100
gccctggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctggggg gccccacctg ggcaggaaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acaggcgatc 250
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgg 300
gactcctggg acgtgaaact gggagccta ggtggaaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
ctttcctccg gggtatggtc atgtacacca gcaaggaccg ctatttctat 450
tttggaaagc ttgtatggca gatctcctct gcctacccca gccaagaggg 500
gcaggtgctg gtggcatct atggccagta tcaactcctt ggcataaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaatc tcacataactc agcaaactca cccgtgggtc gctagggtgg 650
ggtatggggc catccgagct gaggccatct gtgtgggtt ggctgtatgg 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383
<211> 178
<212> PRT
<213> Homo sapiens

<400> 383
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15
Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
20 25 30
Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
35 40 45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
 50 55 60
 Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
 65 70 75
 Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
 80 85 90
 Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
 95 100 105
 Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
 110 115 120
 Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
 125 130 135
 Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
 140 145 150
 Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
 155 160 165
 Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
 170 175

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
 gctgagcgtg tgcgcggtag ggggctctcc tgccctctgg gctccaacgc 50
 agctctgtgg ctgaactggg tgctcatcac ggaaactgct gggctatgga 100
 atacagatgt ggcagctcag gtagccccaa attgcctgga agaatacatac 150
 atgttttcg ataagaagaa attgttaggat ccagttttt ttttaaccgc 200
 cccctccccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
 atgaagatcc tattaccttag gaagatttg atgtttgct gcgaatgcgg 300
 tggggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
 atgttccaaa atcggtccat ctcccaagggt gtccaaatttt tttccctggg 400
 tgtcagcgag ccctgactca ctacagtgc gctgacaggg gctgtcatgc 450
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
 acaaaggatg ggttcaatg taattaggct actgagcgga tcagctgtag 550
 cactggttat agccccact gtcttactga caatgcttcc ttctgccaa 600
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<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

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20 25 30

Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
35 40 45

Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
50 55 60

Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
65 70 75

Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
80 85 90

Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
95 100 105

Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
110 115 120

Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
125 130 135

Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
140 145 150

Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
155 160 165

Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
170 175 180

Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
185 190 195

Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

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215	220	225	
Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys			
230	235	240	
Ile Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu			
245	250	255	
Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Phe Ser Gly			
260	265	270	
Pro Ser Val Phe Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu			
275	280	285	
Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser			
290	295	300	
Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu			
305	310	315	
Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe			
320	325	330	
Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu			
335	340	345	
Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile			
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Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu			
365	370	375	
Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu			
380	385	390	
Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly			
395	400	405	
Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile			
410	415	420	
Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu			
425	430	435	
Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys			
440	445	450	
Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys			
455	460	465	
Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr			
470	475	480	
Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu			
485	490	495	

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 386

ctgggatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 388

gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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gcgatctcaa cgataggat cttgtgttg ccgctattcc agttggtgct 150

ctcgaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

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<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
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Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
20 25 30

Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
35 40 45

His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu
50 55 60

Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
65 70 75

Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
80 85 90

Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
95 100 105

Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
110 115 120

Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
125 130 135

Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
140 145

<210> 391

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 391

cttttcagtg tcacacctcagc gatctc 26

<210> 392

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
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<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
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<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser
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Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu
				20					25					30
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35					40					45
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50					55					60
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65					70					75
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80					85					90
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95					100					105
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110					115					120
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
				125					130					135
Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 396

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<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20				25				30		

Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35				40				45		

Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50				55				60		

Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65				70				75		

Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80				85				90		

Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser
				95				100				105		

Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu
				110				115				120		

Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp
				125				130				135		

Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala
				140				145				150		

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser
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 His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly
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 Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg
 185 190 195
 Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu
 200 205 210
 Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe
 215 220 225
 Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
 230 235 240
 Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly
 245 250 255
 Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala
 260 265 270
 Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp
 275 280 285
 Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
 290 295 300
 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg
 305 310 315
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 Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser
 335 340 345
 Ala Ala Arg Gly Pro Thr Ile Leu
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<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

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<210> 399

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaagggcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caaccccaag ctttaactggg caggagctga ggtgtttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgcag ccacagcttc tgtgagattc gatttctccc cagttcccc 50

gtgggtctga ggggaccaga agggtgagct acgttggctt tctggaagg 100

gaggctatac gcgtcaattc cccaaaacaa gtttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagtg cctgctgttc caggcattac 200

ctgctggca ctaacggcg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttgcagtttttcttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctcttagtct tgccctcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt cagggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcaatcga 600

tgctgcctcc tgcccatatt gctaagactc tatctggaca gggtatcaa 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
gagtcactt gaaaagctgg aaccctcaggc agcagttgtg aaggcttgg 850
gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
acctgcagag gaggcatgac cccaaaccac catctcttta ctgtactagt 1000
cttgcgtgg tcacagtgtt tcttattttt gcattacttg cttccttgc 1050
tgattgtctt tatgcattccc caatcttaat tgagaccata cttgtataag 1100
attttgtaa tatctttctg ctattggata tatttatttag ttaatatattt 1150
tatttatttt ttgctattta atgtattttt tttttactt ggacatgaaa 1200
ctttaaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250
gtatttttat acagtaaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
tgtgaaataa gtttgatgt ggaattgcac atctacotta caattactga 1450
ccatccccag tagactcccc agtcccaataa ttgtgtatct tccagccagg 1500
aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1			5					10					15	

Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20				25					30	

Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35			40						45	

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
				50			55						60	

Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
			65				70						75	

Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
			80			85							90	

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
 95 100 105
 Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
 110 115 120
 Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
 125 130 135
 Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
 140 145 150
 Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
 155 160 165
 Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
 170 175 180
 Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
 185 190 195
 Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
 200 205 210
 Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
 215 220 225
 Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
 230 235 240
 Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln
 245 250 255
 Trp Met Glu Glu Thr Glu
 260

<210> 403

<211> 28

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-28

<223> Synthetic construct.

<400> 403

ctcctgtggc ctccagattt caggccta 28

<210> 404

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 404
agtccctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgtttatcg tttgcgtac tgctaatgt ccgtcccgaa ggaggaggag 50
aggctttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggctaccg tggccagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgcccctat agggaaatgg tgcgcacagc 250
ccttagggatc attgaagagg aaggcttct aaagcttgg caaggagtga 300
cacccgccat ttacagacac gtatgtatt ctggaggatcg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccctttgg aaatcagtca ttggaggat gatggcttgt gttattggcc 450
agtttttagc caatccaaact gacctgtga agttcagat gcaaatggaa 500
ggaaaaagga aactggaaagg aaaaccattt cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttggcag 600
gctgggtacc caatatacaa agagcagcac tggtaatat gggagattta 650
accacttatg atacagtgaa acactacttg gtattgaata caccacttga 700
ggacaatatac atgactcactg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggAACACCA gccgatgtca tcaaaAGCAG aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggctg agaatgaccc cttggtaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc catttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
 20 25 30
 Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
 35 40 45
 Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
 50 55 60
 Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
 65 70 75
 Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
 80 85 90
 Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
 95 100 105
 Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
 110 115 120
 Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
 125 130 135
 Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
 140 145 150
 Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
 155 160 165
 Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
 170 175 180
 Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
 185 190 195
 Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
 200 205 210
 Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
 215 220 225
 Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
 230 235 240
 Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
 245 250 255
 Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
 260 265 270
 Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
 275 280 285
 Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
 290 295 300
 Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407

<211> 31

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-31

<223> Synthetic construct.

<400> 407

cgcggatccc gttatcgctc tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-34

<223> Synthetic construct.

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggacgcgtg ggcgcggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctggata 100

cagcatttaa taaaaaattt atgcttaaga agtaaaaatg gcaggctcc 150

tagataattt tcgttggcca gaatgtaat gtattgactg gagtgagaga 200

agaaaatgtg tggcatctgt tgtgcaggt atattgttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggttatattt ccacattggc tttttcatg 350

ataaaatgtg tatccaatgc tcaggtgaga ggtgataatc atgaaagcgg 400

ctgttagga agaacaggtg ctcgagttt gctttcatt ggtttcatgt 450

tgtatgtttgg gtcacttatt gcttccatgt ggattctttt tggtgcatat 500

gttacccaaa atactgtatgt ttatccggga ctagctgtgt tttttcaaaa 550

tgcaattata ttttttagca ctctgatcta caaatttggaa agaaccgaag 600
agctatggac ctgagatcac ttcttaagtc acatttcct tttgttatat 650
tctgtttgta gatagggttt ttatctctca gtacacattg ccaaatggag 700
tagattgtac attaaatgtt ttgtttcttt acattttat gttctgagtt 750
ttgaaatagt tttatgaaat ttctttatTT ttcattgcat agactgttaa 800
tatgtatata atacaagact atatgaattt gataatgagt atcagtttt 850
tattcctgag atttagaact tgatctactc cctgagccag gttacatca 900
tcttgtcatt ttagaagtaa ccactcttgc ctctctggct gggcacggtg 950
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tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
aggttgcagt gagctgagtt tgccactg cactctagcc tgggggagaa 1200
agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
cataaaaggt tttcagcaag ttgttaactta ttttggccta aaaatgaggt 1350
tttttggta aagaaaaaat atttggctt atgtattgaa gaagtgtact 1400
tttatataat gatttttaa atgcccaaag gactagttt aaagcttctt 1450
ttaaaaagaa ttcctctaattt atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
1 5 10 15

Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
20 25 30

Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
35 40 45

Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
50 55 60

Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
155

<210> 411
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 411
gtttgaggaa gctggatatac 20

<210> 412
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 412
ccaaactcga gcacctgttc 20

<210> 413
<211> 40
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 413
atggcaggct tcctagataa tttcggtgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
gttgcggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50
gcagctggcc cactggcgcc ccgcaacact ccgtctcacc ctctgggccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg cttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cggtggaaag ctgacccaa gccacccttc 300
acctggacag gatgagagtgc tcaggtgtgc ttgcctccct ggccctcata 350
tttgcctatcg tcacgacatcg gatgtttatt cgaagctaca tgagcttcag 400
cataaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtaaaaat ctgcagtggtt gcccggcaacg tcgtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600
tggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctggcacaagg aggcatatcg catgtactct ggagatgtt tgacacccat 700
gaaattcctt aaagaaattc cgggggggtgc actgggtgtg gtggccctt 750
acgacgatcc agggaccaaa atgaacgatcg aaagcagggaa actcttctct 800
gacttgggaa gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaagacc tcagggtaa aagccccttt gagcagttct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcattgcc cccgaagcca ttttaggggtg gctgtggctc 1000
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gcaggcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atgggggtgt ttcgtcaggg actgctgacg 1250
gctggcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300
tatttttgct gggtttgaaa aaaaaaaaaa aaaaaaaaaa 1337

<210> 415
<211> 224
<212> PRT
<213> Homo sapiens

<400> 415
Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
1 5 10 15
Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
20 25 30
Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
35 40 45
Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
50 55 60
Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
65 70 75
Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
80 85 90
Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
95 100 105
Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
110 115 120
Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
125 130 135
Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
140 145 150
Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
155 160 165
Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
170 175 180
Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
185 190 195
Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
200 205 210
Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
215 220

<210> 416
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccca agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgctcgc tctctctc tctctctcac tcctccctcc 200
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtcccct 250
gcaccccttc ctgggacact atgttgttct ccgcctcct gctggaggtg 300
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgaggccc 350
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagccca cggatatgac cagcctggca ccgagccctt 500
ggacctgcac aacaatggcc acacagtgc aactctctcg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgccc gctccacctg 600
cactgggtc agaaaggatc cccaggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggt gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatacgat atgaacacat 800
tctgagtacac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccc aacagctggg gcagtacttc 900
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
gacagtttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
ttcaggggac attgttctcc acagaagagg agccctotaa gcttctggta 1050
cagaactacc gagcccttca gcctctcaat cagcgcattgg tcttgcttc 1100
tttcatccaa gcaggatcct cgataaccac aggtgaaatg ctgagtctag 1150
gtgttaggaat cttgggttggc tgtctctgcc ttctcctggc tttttatttc 1200
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtgg 1250
cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
gggtgttagga tctggccaga aacactgttag gagtagtaag cagatgtcct 1400
ccttcccctg gacatctctt agagaggaat ggacccaggc tgtcattcca 1450
ggaagaactg cagagccttc agcctctcca aacatgttagg aggaaatgag 1500
gaaatcgctg ttttgttaat gcagaganca aactctgttt agttgcaggg 1550
gaagtttggg atatacccca aagtccctcta cccccctcaact tttatggccc 1600
tttccttaga tataactgcgg gatctctcct taggataaaag agttgctgtt 1650
gaagttgtat attttgatc aatatatttg gaaattaaag tttctgactt 1700
t 1701

<210> 423
<211> 337
<212> PRT
<213> Homo sapiens

<400> 423
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
1 5 10 15
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
20 25 30
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
35 40 45
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
50 55 60
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
65 70 75
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80	85	90
Pro Ser Thr Leu Tyr Leu Gly Gly Leu Pro Arg Lys Tyr Val Ala		
95	100	105
Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly		
110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His		
125	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala		
140	145	150
Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu		
155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His		
170	175	180
Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro		
185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe		
200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val		
215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln		
230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro		
245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn		
260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr		
275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly		
290	295	300
Cys Leu Cys Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile		
305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser		
320	325	330
Ala Gln Ala Thr Thr Glu Ala		
335		

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgtc 18

<210> 426
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<213> Artificial

<220>
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<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgtc tggccattat tgtc 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaaccca tgataacccta ctgaacacccg aatccccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
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acatTTTgcc tcgtggaccc aaaggttagca atctgaaaca tgaggagttac 100
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaca 200
ctaccaaacc aacagcagtc aaatcaggc tttccttctt taagtctgat 250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaatc 300
ctgctgcagg aatgacacct ggtacccaga cccaccatt gaccctggga 350
gggttgaatg tacaacagca actgcaccca catgtgttac caattttgt 400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
aaatcttcac gagcctcatc atccattcct tttcccgaa aggcatcctg 500
cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
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gcctcccaac tcccagtggc acagatgacg actttgcagt gaccacccct 650
gcagggatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700
agcaaatgga attcagtaag ctgtttcaaa tttttcaac taagctgcct 750
cgaatttggt gatacatgtg aatctttatc attgattata ttatgaaata 800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
gaaaatattc ttgaaatttc agaaaatatg ttctatgttag agaatcccaa 900
cttttaaaaaa caataattca atggataaat ctgtcttga aatataacat 950
tatgctgcct ggatgatatg catattaaaa catatttggaa aaactggaaa 1000
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

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1				5				10					15	
Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
	20				25								30	
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Ser	Asn	
			35					40					45	
Gln	Val	Phe	Pro	Ser	Leu	Ser	Ile	Pro	Leu	Thr	Gln	Met	Leu	
			50				55					60		
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
			65				70					75		

Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn
 80 85 90
 Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr
 95 100 105
 Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro
 110 115 120
 Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly
 125 130 135
 Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp
 140 145 150
 Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln
 155 160 165
 Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp
 170 175 180
 Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His
 185 190 195
 Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln
 200 205
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 <211> 1257
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 ccgcctccag ctccgcgtg cccggcagcc gggagccatg cgaccccagg 150
 gccccgcccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
 ctgcagctgc cccgcgcgtc gagcgcctct gagatcccc agggaaagca 250
 aaaggcgcag ctccggcaga gggaggttgt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacggag ccctggggcc 350
 aatgttattc cgggtacacc tggatccca ggtcggatg gattcaaagg 400
 agaaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
 actacaagca gtgttcatgg agttcattta attatggcat agatcttggg 500
 aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgtcttaag 550
 agttttgttc agtggctcac ttccggctaaa atgcagaaat gcatgctgtc 600
 agcgttggta tttcacatc aatggagctg aatgttcagg accttccc 650

attgaagcta taattttattt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgactt cttctgtgga aggactttgt gaaggaaattg 750
gtgctggatt agtggatgtt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagttctc gcatcattat 850
tgaagaacta caaaaataaa tgcttaatt ttcatttgc acctctttt 900
ttattatgcc ttgaaatggt tcacttaat gacattttaa ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgttttaa atcttagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttggtt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttgaaatatt gttgtggtot tttgtttttt 1150
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<211> 243

<212> PRT

<213> Homo Sapien

<400> 431

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Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30

Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45

Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60

Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75

Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90

Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105

Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120

Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
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Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

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atgacgctcg tccaaggcca c 21

<210> 435

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<400> 435
cccacctgta ccaccatgt 19

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<400> 436
actccaggca ccatctgttc tccc 24

<210> 437
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aagggctggc attcaagtc 19

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tgacctggca aaggaagaa 19

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cagccaccct ccagtccaag g 21

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<400> 440
gggtcgtgtt ttggagaga 19

<210> 441
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<400> 442
tcctccatca cttcccctag ctcca 25

<210> 443
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<400> 443
ctggcaggag ttaaagtcc aaga 24

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<400> 444
aaaggacacc gggatgtg 18

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<400> 446
caattctgga tgaggtggta ga 22

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caaagcgcca agtaccggac c 21

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<210> 457
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<220>
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<210> 458
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tagcagctgc ccttggta 18

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aacagcaggt gcgactcatc ta 22

<210> 460
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<220>
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<400> 460
tgctaggcga cgacacccag acc 23

<210> 461
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tggacacgtg gcagtgg 18

<210> 462
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gccccagagtc ccacttgt 18

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<210> 470
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<210> 471
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<400> 471
cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
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tcagggtcta catcagccctc ctgc 24

<210> 473
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aaggccaagg tgagtccat 19

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<400> 475
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<210> 476
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<400> 476
gggaggctta taggccaaat ctgg 24

<210> 477
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<400> 477

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